

COMPOSITIONS AND METHODS FOR TREATING OR PREVENTING HIV INFECTION

This application claims the benefit of U.S. Provisional Application Nos.
5 60/491,258 filed July 31, 2003, 60/493,767 filed August 11, 2003, 60/496,908 filed
August 22, 2003, and 60/501,832 filed September 11, 2003, which are hereby
incorporated by reference in their entirety.

BACKGROUND OF THE INVENTION

10 Acquired Immune Deficiency Syndrome ("AIDS") is one of the most serious
health threats confronting the human population today. AIDS is caused by a virus
known as human immunodeficiency virus ("HIV") which presently includes HIV-1
and HIV-2. Over 40 million people are estimated to be living with HIV/AIDS.
Current projections suggest that an additional 45 million people will become infected
15 between 2002 and 2010. So far, it is believed that more 25 million people have died
from AIDS.

Since its emergence in the 1970s, HIV has produced a continually growing
global pandemic, and it has, thus far, defied all attempts to produce an effective
vaccine. Although a number of drugs have been developed to treat the disease, all
20 have limited usefulness, serious side effects, a high potential for resistance, and none
have been identified so far which can cure or prevent it. HIV vaccine research has
expanded over recent years, but success so far using HIV-based components has been
limited. See, e.g., Graham et al., *J. Inf. Disease.*, 166:244-252, 1992; Belshe et al., *J.*
Inf. Disease., 183:1343-52, 2001; Horton et al., *J. Virol.*, 76:7187-7202, 2002; Gilbert
25 et al., *Vaccine*, 21:2933-2947, 2003.

DESCRIPTION OF DRAWINGS

FIG. 1 (A-C). Comparison of cells from vaccinated versus non-vaccinated subjects,
infected with the macrophage (CCR5) tropic HIV. A. A comparison of the mean +
30 standard error measurement of the vaccinated versus non-vaccinated groups in
cultures without autologous serum. (*, $p < 0.05$) B. A comparison of the mean +

standard error measurement of the vaccinated versus non-vaccinated groups in cultures with autologous serum (*, $p < 0.05$; **, $p < 0.01$). C. Comparison of the mean + standard error measurement of cells from vaccinated versus non-vaccinated subjects, infected with the T-cell (CXCR4) tropic HIV.

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DESCRIPTION OF THE INVENTION

The present invention provides methods and compositions for treating and/or preventing HIV infection in a subject in need thereof. It features the use of poxviruses for therapy, prophylaxis, and diagnosis of HIV, as well as for any other
10 medical or veterinary use associated with HIV and homologous viruses. The invention also provides for the use of poxviruses in the discovery of new agents to prevent and/or treat HIV infection.

A poxvirus or a component thereof, can be used to treat and/or prevent infection caused by any virus, preferably a lentivirus, such as HIV, that uses a CCR5
15 chemokine receptor for its infection of cells. This includes, but is not limited to, e.g., HIV-1 (e.g., clades A, B, C, D, and G, R5 and R5X4 viruses, etc.), HIV-2 (e.g., R5 and R5X4 viruses, etc.), simian immunodeficiency virus (SIV), simian/human immunodeficiency virus (SHIV), feline immunodeficiency virus (FIV), bovine immunodeficiency virus (BIV) (Wright et al., *Vet. Res. Commun.*, 26:239-50, 2002),
20 HTLV-1, HTLV-2, etc. It can be used as a vaccine, adjuvant, therapeutic agent, in combination with other agents, or in any suitable manner to treat and/or prevent such infections.

Any poxvirus can be used in accordance with the present invention, including, but not limited to, orthopoxvirus, parapoxvirus, avipoxvirus, capripoxvirus,
25 leporipoxvirus, suipoxvirus, etc. Orthopoxvirus, include, e.g., buffalopox, camelpox, cowpox, monkeypox, rabbitpox, raccoon pox, tatera pox, canarypox, fowlpox, vaccinia, variola, and vole pox. Vaccinia virus is the prototype of the genus Orthopoxvirus for the desired effects, but other poxviruses can be used in its place. Thus, although the disclosure below may be written in terms of vaccinia, any poxvirus
30 can be utilized in accordance with the present invention.

Vaccinia is a double-stranded DNA (deoxyribonucleic acid) virus. All strains, derivatives, variants, mutations, naturally-occurring strains, genetically-engineered, recombinant, etc., of vaccinia can be used in accordance with the present invention. For more information on vaccinia and other poxvirus, see e.g., *Virology*, Fields et al.,
5 Volume 2, Chapters 74-75, Raven Press, 1990.

An amount of the poxvirus, such as vaccinia virus, can be administered to a subject in a quantity which is effective to achieve a therapeutic or prophylactic effect. The term "poxvirus," "vaccinia virus," etc., indicates that the virus (genome and protein coat) is administered to a subject. It can be administered in any effective
10 form, including, e.g., as a live virus, as a live-attenuated virus, as a replication-deficient virus, as a viral extract not having any live viral particles, etc. Compositions comprising a poxvirus can be produced and utilized in any suitable manner, including, e.g., recombinant, naked DNA technology, etc.

The term "treating" is used conventionally, e.g., the management or care of a
15 subject for the purpose of combating, alleviating, reducing, relieving, improving, eliminating, etc., one or more signs or symptoms associated with HIV infection. Treatment includes delaying the progression of HIV and its associated symptoms, thereby extending the life expectancy of an infected subject, and/or delaying or reducing the onset of symptoms associated with HIV infection. Treating can involve
20 inhibiting, reducing, diminishing, etc., the replication and other events in the life cycle of the HIV virus.

The term "preventing" HIV infection indicates that a subject's susceptibility to HIV infection upon exposure to the virus is reduced or diminished as a result of the administration of the poxvirus. The subject's resistance to HIV infection is increased
25 or improved by the poxvirus treatment since s/he is less likely to become infected by the virus. Any amount of improved resistance is useful, e.g., greater than 5-fold, greater than 7-fold, greater than ten-fold, etc., and any such improvement can be regarded as prevention.

A poxvirus, or component thereof, used in the present invention can be
30 prepared routinely, or obtained from commercial sources. Attenuated strains are preferred. Attenuated strains are less able to cause disease, and are considered less virulent and weakened as compared to strains that are not attenuated.

Any strain of vaccinia virus, or components thereof, can be utilized to achieve a prophylactic and/or therapeutic effect, including, but not limited to, e.g., strains available from the ATCC, ECACC, or other virus collections, replication-competent, replication-deficient, non-replicating, attenuated strains, modified vaccinia Ankara (MVA), vaccinia virus Ankara, NYVAC (ATCC No. VR-2559) replication-deficient vaccinia viruses, VV Copenhagen, VV Western Reserve, VV Wyeth (ATCC No. VR325), Elstree, strains deficient in vCCI (Reading et al., *J. Immunol.*, 170:1435-42, 2003), and/or vGF, strains comprising one or more copies of the 17K myristyloprotein, poxvirus strains, CCR5-dependent poxvirus strains, etc. Dryvax®, a vaccinia (smallpox) vaccine currently licensed in the United States, is a lyophilized, live-virus preparation of infectious vaccinia virus (Wyeth Laboratories, Inc., Marietta, Pennsylvania). Other strains which have been used include, but are not limited to, e.g., Lister, Bordeaux, Paris, Massachusetts 999, New York, Temple of Heaven, Patwadangar, Ikeda, Bern, Vienna, Bohemia, Finland, Hamburg, Budapest, Aosta, Spain, Sweden, B-51, Tashkent, EM-63, LE-IVP (Lister), etc. See, also, *Smallpox and its Eradication*, Fenner et al., WHO, Geneva, 1988, e.g., Chapter 11. Other strains include, e.g., MVA-BN (modified vaccinia Ankara – Bavarian Nordic) (ECACC V00083008; WO 02/42480), MVA-Vero (US 20030013190), MVA-NH, MVA 572 (ECACC V94012707), LC16m8, and ACAM1000 (ATCC Deposit No. PTA-3321; WO 02/085411). Any strain of canarypox can be utilized as well, including attenuated canarypox virus such as, e.g., ALVAC (ATCC No. VR-2547).

Deposited strains also include, e.g., ATCC Nos. VR-117 (CL), VR-118 (Lederle-Chorioallantoic), VR-119 (WR (Mouse Neurotropic), VR-1354 (WR (NIH TC-adapted), VR-1431 (P-4), VR-1441 (IHD-W), VR-1508 (Modified vaccinia virus Ankara (MVA)), VR-1536 (New York City Department of Health Laboratories (Wyeth-calf adapted)), VR-1549 (Elstree (Lister Vaccine)), VR-156 (IHD), VR-2010 (AS), VR-2031 (Vtk-79), VR-2034 (S-variant), VR-2042 (vP-7), VR-2043 (vP-9), VR-2292 (SLZ103[recombinant Vaccinia virus (WR)]), VR-2379 (Rpmuhr+ [recombinant of Utrecht strain Rpuhr23]), VR-2589 (VVtm1:hPC1 [recombinant Vaccinia virus, in vitro construct]), VR-302 (Brighton), VR-3103 (IHD-W Dts 16 [Vaccinia ts-mutant]), VR-3109 (IHD-W Dts 46 [Vaccinia ts-mutant]), VR-3110 (IHD-W Dts 2 [Vaccinia ts-mutant]), VR-3113 (IHD-W Dts 17 [Vaccinia ts-mutant]),

VR-3121 (IHD-W Dts8 [Vaccinia ts-mutant]), VR-3126 (IHD-W Dts 33 [Vaccinia ts-mutant]), VR-3129 (IHD-W Dts 48 [Vaccinia ts-mutant]), VR-3130 (IHD-W Dts 4 [Vaccinia ts-mutant]), VR-3139 (IHD-W Dts 50 [Vaccinia ts-mutant]), VR-3142 (IHD-W Dts 10 [Vaccinia ts-mutant]), VR-3144 (IHD-W Dts20), VR-3147 (IHD-W Dts 35 [Vaccinia ts-mutant]), VR-3148 (IHD-W Dts 40), VR-3154 (IHD-W Dts71 [Vaccinia ts-mutant]), VR-3160 (IHD-W Dts52 [Vaccinia ts-mutant]), VR-3161 (IHD-W Dts 57), VR-3165 (IHD-W Dts 77), VR-3166 (IHD-W Dts 82), VR-3169 (IHD-W Dts97 [Vaccinia ts-mutant]), VR-3175 (IHD-W Dts 78 [Vaccinia ts-mutant]), VR-3176 (IHD-W Dts 83 [Vaccinia ts-mutant]), VR-3178 (IHD-W Dts 93 [Vaccinia ts-mutant]), VR-3196 (IHD-W Dts 95 [Vaccinia ts-mutant]), VR-587 (Yaba monkey tumor virus deposited as Yaba monkey tumor virus, Yatapoxvirus (Roswell Park-Yohn)), VR-838 (Raccoonpox virus, Orthopoxvirus (Herman)).

A vaccinia virus is a preferred poxvirus in accordance with the present invention, but other poxviruses can also be used to treat and/or prevent HIV. For example, any poxvirus which expresses a gp120-like or TAT-like polypeptide, or which depends on CCR5 for entry into a cell can be used in accordance with the present invention.

Vaccinia virus can be administered to subjects according to any regimen which is effective for treating and/or preventing HIV infection. The particular dosages (i.e., effective amounts), and number and frequency of vaccinations can be determined routinely.

An effective amount of virus, or virus component, is the quantity of virus, or virus component, which is useful to achieve the desired purpose, e.g., to treat and/or prevent HIV infection. These amounts can be determined routinely. Effective amounts can be the same or less than the amounts currently used to achieve pox immunity with a pox vaccine. For example, Dryvax™ is commonly used at a potency of 100 million pock-forming units (pfu)/ml for primary vaccination for smallpox. Any effective amount can be used in accordance with the present invention, e.g., about 10^5 - 10^9 pfu/ml. The quantities of the particular virus which is utilized can be adjusted and determined routinely, e.g., to eliminate or reduce adverse reactions associated with the virus, as well as depending on the health of the patient receiving the treatment.

The specific dose level and frequency of dosage may vary, and can depend upon a variety of factors, including the activity and state of the specific poxvirus, e.g., whether it is live, heat-inactivated, attenuated, etc., its metabolic stability and length of action, rate of excretion, mode and time of administration, and the age, body weight, general health, gender, diet, and particular condition of the subject undergoing treatment or prevention.

Poxvirus can be administered in any form by any effective route, including, e.g., oral, parenteral, enteral, intraperitoneal, topical, transdermal (e.g., using any standard patch), ophthalmic, nasally, local, non-oral, such as aerosol, spray, inhalation, percutaneous (epidermal), subcutaneous, intravenous, intramuscular, buccal, sublingual, rectal, vaginal, intra-arterial, mucosal, and intrathecal, etc. It can be administered alone, or in combination with any ingredient(s), active or inactive.

Any subject can be administered a poxvirus in accordance with the present invention, including subjects who have been exposed to HIV, but have not yet developed HIV infection, as well as subjects who have progressed to one or more of the clinical symptoms of HIV infection (e.g., AIDS). In addition to treating and/or preventing HIV infection in humans, a poxvirus can be used to treat other organisms (e.g., non-human primates, cats, etc.) infected with HIV, or HIV-related viruses, such as SIV, SHIV, or FIV. Thus, subjects who can be treated include, e.g., mammals, humans, monkeys, apes, chimpanzees, gorillas, cats, dogs, mice, rats, etc.

Subjects, who have been exposed to HIV virus, or who are at risk for developing the disease, are particular candidates for poxvirus vaccination. For instance, a subject who has not yet tested positive, but has been exposed to HIV, can be administered vaccinia virus as a prophylactic/therapeutic approach. Individuals at high-risk for the disease, such as sexually-active individuals, subjects in parts of the world where HIV infection is high, subjects receiving blood and/or other invasive medical procedures, can also receive vaccination to increase their resistance to HIV infection.

In addition to administering the whole poxvirus, components of it can also be administered in accordance with the present invention. By the phrase "component," it is meant any part of the virus, which is less than the whole virus genome, including

particular nucleic segments of its genome, as well as any product which is produced using the viral genome. This includes modifications to polypeptides encoded for by the virus.

Components include polypeptides comprising the virus, such as envelope
5 proteins, processing enzymes, structural proteins, nucleic acid synthesis enzymes, glycoproteins, carbohydrates, lipids, antigens or antigenic fragments of the virus, etc. Also included are nucleic acid fragments of the whole genome, including fragments comprising complete gene sequences, control sequences, etc.

Components includes one or more of the over about 198 open reading frames
10 (ORF) and about 268 genes that have been identified in vaccinia and other poxvirus. Components include one or more of the genes and products thereof described in, but not limited to, Antoine et al., *Virology*, 244:365-396, 1998, and Goebel et al., *Virology*, 179(1):247-266, 1990 for vaccinia virus; Willer et al., *Virology*, 264(2):319-43, 1999 for Leporipoxvirus Shope fibroma virus (SFV); Cameron et al., *Virology*,
15 264(2):298-318, 1999 for myxoma virus; Shchelkunov et al., *Virology*, 297(2):172-94, 2002 for monkeypox virus; Shchelkunov and Totmenin, *Virus Genes*, 9(3):231-45, 1995 for variola, Massung et al., *Virology*, 201(2):215-40, 1994. For example, the polypeptide coding for the 17K myristylprotein, and which has amino acid sequence homology to gp120, can be used alone or in combination with other antigens, etc., in
20 accordance with the present invention. See, e.g., Antoine et al., 1998; Barrett et al., *Seminars in Immunol.*, 13:73-84, 2001. See, also Tables 1 (from Goebel et al., *Virol.*, 179:247-266, 1990) and 2 (from Antoine et al., *Virol.*, 244:365-396, 1998). Moreover, one or more of the aforementioned genes and open reading frames can be deleted from a vaccinia virus, e.g., to eliminate a toxic or other undesirable effect of an
25 administered virus.

A useful composition can comprise one of the components of a poxvirus, including one or more of the components described in Tables 1 and 2. These can be individual purified and then combined into a therapeutic or prophylactic composition, or extracts can be prepared from viral particles and treated as desired. The individual
30 components can be purified from the viral particles, or produced recombinantly, e.g., where a target gene is cloned, expressed in a host cell under conditions where the polypeptide is manufactured by the cell, and separating and purifying the polypeptide

accordingly to conventional methods. Components can also be administered as naked DNA. See, e.g., U.S. No. 6,413,942.

The therapeutic and/or prophylactic effect achieved with the poxvirus can be independent of an immunological response to it. For example, the purpose of ordinary smallpox vaccination is to elicit an immune response by the host. This response is both humoral and cellular, involving the generation of specific antibodies and immune cells (such as T-cells, cytolytic or cytotoxic T lymphocytes, etc.) which protect a host from future invasion by the smallpox virus. While the present invention is not bound by any mechanism through which the poxvirus achieves its therapeutic and/or prophylactic effect, it can be mediated through a pathway separate from the immune response and not require cellular or humoral immunity. For example, poxvirus, or a component thereof, can directly block or inhibit the ability of a HIV to infect a cell. In this respect, the poxvirus, or component of it, acts as an antagonist, blocker, etc., of HIV's ability to infect target cells. HIV usually activates a G-protein-coupled signal pathway cascade. Poxvirus can interfere with this pathway or modify it such a way that the cell is more difficult to infect, thereby increasing its resistance to the HIV virus. Consequently, the effective amounts of a poxvirus, or component thereof, can differ from the amounts that are ordinarily used when the objective is to achieve a humoral and/or cellular immune response.

Vaccination with vaccinia can be associated with adverse reactions. Those at highest risk include, e.g., pregnant women, immunocompromised patients (e.g. HIV-positive), and persons who have atopic dermatitis or eczema. Strains which are attenuated or otherwise modified to reduce adverse effects are especially useful in accordance with the present invention, e.g., for administration to persons at risk for adverse effects.

Modified strains of vaccinia can be utilized that are deficient, mutated, engineered, etc., in one or more of the about 198 open reading frames (ORF) and/or about 268 genes that comprise vaccinia (depending on the strain or variant). In addition, genes can be inserted into vaccinia, including, one or more copies of a vaccinia gene of interest (e.g., 17K myristylprotein, vCCI), and/or genes coding for all or part of an HIV proteins, such as gp120 or gp40.

The present invention also provides methods of treating and/or preventing HIV infection in a subject in need thereof, comprising, e.g., administering multiple doses of a poxvirus, or components thereof, to a subject, wherein each dose is administered at a time interval from the previous dose, and are effective to maintain a therapeutic effect, or to maintain protection against HIV infection. As discussed above, a dose of the poxvirus, or component thereof, is the amount of virus which is useful for accomplishing the therapeutic or prophylactic effect. More than one dose can be administered to the subject in order to maintain the therapeutic efficacy of the treatment, or to maintain protection against HIV infection. For example, smallpox immunization is usually achieved by a single vaccination with a booster every 5-10 years. To maintain protection against HIV, more frequent vaccination can be used, e.g., multiple times a year; at least twice a year, yearly, every two years, every three years, more than once every less than five years, more than once every less than ten years, etc. The periods between the separate and sequential vaccinations can be referred to as "time intervals." These intervals can be spaced apart by any desired time period which is effective to maintain protection or therapeutic efficacy in treating an infected subject. The intervals can be predetermined or preset, where they are already specified, or they can be determined by monitoring the progress of a subject, e.g., using blood serum to measure poxvirus antibody titer, or HIV titer in an infected subject. The frequency of vaccination utilized to achieve efficacy may vary depending upon multiple factors, including, e.g., person-to-person variations in the immune system, the stage of HIV infection, the potency of the virus or vaccine, etc, and may be as often as every 3 months to once every 5 years.

The present invention also provides methods of treating and/or preventing lentivirus infection in a subject in need thereof, comprising: administering an effective amount of a poxvirus or component thereof, wherein said amount is effective to treat and/or prevent lentiviral infection, with the proviso that a lentivirus nucleic acid, such as HIV, is not contained in the poxvirus genome. This excludes, e.g., a poxvirus which is utilized as a vector to administer HIV nucleic acid, such as when HIV nucleic acid is inserted into the poxvirus genome.

The present invention also provides methods of identifying a component of a poxvirus, or a poxvirus-associated agent, which interferes with HIV infection, and

components and agents identified thereby. Interfering with HIV infection indicates that the agent or component decreases, reduces, diminishes, lessens, etc., the ability of a susceptible cell or organism to become infected with HIV virus as compared to the same cell or organism in the same conditions, but in the absence of the agent or
5 component. Interference with HIV infection can occur at any level, e.g., by blocking the ability of HIV to attach to its receptor(s) on a cell, by blocking the ability of HIV to be taken into a cell, by blocking viral function once inside the cell, by blocking viral infection, etc. The invention is not limited by the mechanism through which HIV interference is achieved. By interfering with HIV infection, the cell's or
10 organism's resistance to HIV is increased.

These methods can involve one of more of the following steps in any effective order, e.g., (1) contacting a cell or organism which is susceptible to HIV infection with poxvirus, or a component thereof, or a poxvirus-associated agent, (2) contacting
15 said cell or organism with HIV under conditions effective for said HIV to infect said cell or organism, and, (3) (a) determining whether said cell or organism is resistant to HIV infection, whereby said agent is identified as interfering with HIV infection, or (3) (b) identifying the poxvirus, or component thereof, which confers resistance to HIV infection. The term "organism" as used herein indicates a fully-gestated animal.

The method can also involve a step of identifying the poxvirus, or a
20 component thereof, as the agent which confers resistance to HIV infection. Identifying the poxvirus, or component thereof, which confers resistance to HIV infection, indicates that the poxvirus is positively determined or ascertained to provide protection or resistance against HIV. This indicates a positive result in the method.

25 Agents can be tested for their ability to interfere with HIV infection in any suitable system, including whole animals and cell culture. Animal cells useful in the present invention are those which are susceptible to HIV infection, i.e., they are capable of being infected by the HIV virus. They can be naturally-susceptible, or genetically-engineered to confer susceptibility, e.g., by expressing HIV receptor
30 (CCR5, CD4, etc.), or by grafting on the human immune system. Any methods for testing whether a cell or organism is infected with HIV can be used, e.g., measuring

anti-HIV antibody titer (e.g., gp120 antibodies), reverse transcriptase protein or nucleic acid, or any other polypeptide or nucleic acid.

Any suitable animal model for testing the efficacy and dosage of a poxvirus (or component thereof) can be used in accordance with the present invention. These
5 include, but are not limited to, e.g., SCID mice reconstituted with human immune system components (e.g., peripheral blood lymphocytes) [e.g., Zhang et al., *Proc. Natl. Acad. Sci.*, 93:14720-14725, 1996, using SCID.bg mice], chimpanzees infected with HIV-1, macaque monkeys infected with SIV, HIV2, or chimeric SIV/HIV [e.g., Johnson, *Curr. Opin. Immunol.*, 8(4):554-560, 1996], cats infected with feline
10 immunodeficiency virus, HIV-1 transgenic mouse model [e.g., mice which have integrated molecular clone pNL4-3 containing 7.4 kb of the HIV-1 proviral genome deleted in the gag and pol genes (Dickie et al., *Virology*, 185:109-119, 1991; transgenic mice carrying an HIV provirus, optionally with deletion of one or more HIV genes (Tinkle et al., *J. Clin. Invest.*, 100(1):32-9, 1997)], HIV-1 transgenic rat
15 model, human CD4 transgenic rat model, horse infected with EIAV, sheep infected with visna virus, goats infected with CAEV, etc. See, also, *The Retroviridae*, J. A. Levy, ed., Plenum Press, 1993, e.g., Chapters 3, 4, and 5.

A vaccinia virus-associated agent is any substance which is produced in response to a vaccinia infection, or in response to inhalation, injection, ingestion, etc.,
20 of any vaccinia virus, or component thereof. This substance can be present in a culture medium in which cells exposed to vaccinia have been cultured, or can be present in blood serum when harvested from an organism exposed to vaccinia. The present invention provides compositions which comprise such substances.

The invention also provides combinations of pharmaceutical agents for
25 treating and/or preventing HIV, e.g., poxvirus, or a component thereof, and an agent which is used to treat HIV, such as a protease inhibitor or a reverse transcriptase inhibitor. Examples of the latter classes of drug, include, but are not limited to, saquinavir, ritonavir, indinavir, nelfinavir, amprenavir, lopinavir, atazanavir, fosamprenavir, tipranavir, AZT, ddI, ddC, ddT, 3TC, nevirapine, delavirdine, etc.
30 The active agents can be present in the same dosage unit (e.g., a composition), or can be used as separate dosage units.

In addition, a poxvirus, such as vaccinia, can be administered in combination with HIV nucleic acid. The HIV nucleic acid can be physically joined to the poxvirus genome, or it can be administered as a separate component. For example, HIV nucleic acid (e.g., coding for gp120 or another viral antigen) can be administered at the same time as a poxvirus, but as a physically separated entity, or it can be administered at subsequent times after receiving only poxvirus) as part of a regimen for treating and/or preventing HIV infection.

The present invention also provides methods of making a poxvirus composition for conferring resistance to HIV infection or treating HIV infection, comprising, one or more of the following steps in any effective order, e.g., preparing a composition comprising poxvirus, or a poxvirus component thereof, and/or identifying that the poxvirus, or component thereof, confers resistance to, or treats, HIV infection. As mentioned earlier, the identifying step indicates obtaining a positive result in finding that the poxvirus (e.g., vaccinia), or component thereof, provides resistance, protection, treatment, etc., against the HIV virus.

The preparation of a poxvirus composition can be carried out routinely, e.g., according to conventional methods used for vaccine manufacture. Preparing includes culturing poxvirus, isolating poxvirus, putting poxvirus into a form suitable for administration (oral, injection, nasal, etc.), making poxvirus components recombinantly, etc. The prepared poxvirus (or components of it) can be assayed for its ability to confer resistance to HIV infection to an organism challenged with it or provide a therapeutic effect. By this, it is meant that a sample of the prepared composition is tested to determine its titer, concentration, potency, etc., in making a subject, to whom it is administered, "resistant" to the HIV virus, or for its therapeutic effect. The assay step can be carried out on every batch, or only selected batches, etc. A purpose of this step is, e.g., to confirm that the manufactured poxvirus possesses an anti-HIV activity for which it is to be administered. Any suitable assay or testing method can be utilized, e.g., in vitro methods of evaluating its efficacy or potency. For instance, the determining step can involve, e.g., challenging said organism, or cells derived from it, with infectious HIV, and detecting the expression in said organism or cells of gp120, HIV reverse transcriptase, p24, infectious HIV particles, and/or HIV nucleic acid. By "challenge" it is meant the cells or organism are placed

in contact with the HIV virus under conditions which are effective to become infected by it. These conditions will vary, depending upon how the assay is specifically accomplished.

When poxvirus is administered to a host, it can elicit a cellular response that is responsible or associated with the host's subsequent ability to resist HIV infection and/or treat HIV infection. This response can be measured, and used as index or marker to assess the efficacy of the poxvirus, and/or to determine effective amounts of it for the desired purpose (i.e., treating or preventing HIV infection). The appearance of one or more of the following "markers" can be modulated (e.g., elicited, stimulated, down-regulated, up-regulated, etc) by poxvirus, and associated with its anti-HIV effect, thereby making the marker useful as an indicator of poxvirus efficacy. By the term "marker," it is meant any measurable response to a poxvirus, including its effect on HIV's ability to infect and replicate in a cell, as well as on the host's immune system and the cells which comprise it. These markers, include, but are not limited to; one or more of the following agents, activities, responses, pathways, etc.:

- CD4 expression, e.g., measuring the amount of CD4 present in a cell-type that is susceptible to HIV infection
- HIV coreceptor expression, e.g., CCR5 or CXCR4 chemokine receptor, including its cell-surface expression
- Cytokine receptors
- Virus-specific CTLs (cytolytic or cytotoxic T-cells, including CD8+ T-cells) which are capable of lysing HIV infected cells (cells can be co-infected with poxvirus and HIV, or infected by HIV alone)
- CD8 cells
- Cytokines, including mediators and regulators of innate immunity, such as interferons, type I interferon, interleukins, interleukin-15, interleukin-12, tumor necrosis factor, interleukin-1, interleukin-6, interleukin-10, etc.; and mediators and regulators of specific immunity, such as interleukins, interleukin-2, interleukin-4, transforming growth factor-beta, interferon-gamma, lymphotoxin, interleukin-5, etc.
- Chemokines (a large family of structurally homologous cytokines, that, e.g., stimulate leukocyte motility and directed movement), including, but not limited to,

the C-C and C-X-C families. Examples of chemokines, include, but are not limited to, e.g., interleukin 8, Gro, platelet basic protein, epithelial-derived neutrophil attractant 78, platelet factor 4, interferon-gamma-induced protein 10, stromal cell-derived factor-1, monocyte chemotactic proteins 1, 2, and/or 3, RANTES, monocyte inflammatory protein 1-alpha and 1-beta ("MIP"), eotaxin, lymphotaxin, etc.

- Th1/Th2 phenotype and cytokine secretion pattern. Effector T-cells (e.g., CD4+ helper T-cells) can be categorized, on the basis of the cytokines they secrete, into Th1 and Th2 cells. Th1 cells secrete, e.g., interferon-gamma, lymphotoxin-alpha, TNF-beta, IL-2, IL-10, and CCR5 ligands, such as RANTES and MIPs. Th2 cells secrete, e.g., IL-4, IL-5, IL-6, IL-9, IL-10, IL-13, etc. Th1 and Th2 cells also include resting, but polarized T-cells (i.e., committed to a Th type). In addition to cytokine production profiles, there are a number of cell surface markers that can be used to differentiate between Th1 and Th2 subtypes. For example, Th1 cells express both components of IL-12 receptor chains (beta1 and beta2), while Th2 cells exhibit IL-12R-beta1. Th2 cells exhibit both IFN-gamma receptor chains (a and b), while Th1 cells express IFN-gamma-R-alpha. Th2 cells appear to express a fully functional IL-1 receptor, and ST2L/T1, an IL-1R-like molecule, is found on Th2 cells. Chemokine receptors CXCR-3 and CCR-5 are also characteristic of Th1 cells, while CXCR-4, CCR-3, CCR-4, CCR-7 and CCR-8 are associated with Th2 cells. CD30, a member of the TNF superfamily, is associated with Th2 cells. The Th1/Th2 pattern can be polarized by poxvirus administration, resulting in a phenotype that favors the secretion, etc., of cytokines that inhibit HIV infection and/or render cells resistant to infection. One or more of the aforementioned molecules can be utilized as markers of poxvirus efficacy

- Antibodies that specifically recognize HIV, e.g., neutralizing antibodies
- Antibodies that specifically recognize poxvirus
- Complement control protein. Vaccinia virus encodes a secreted complement control protein (VCP, 35-kDa) protein with sequence homology to the SCR-containing complement control protein superfamily. It binds C3b and C4b, and interferes with the complement cascade by providing cofactor activity for the cleavage of C3 and C4 by factor I, and by accelerating the decay of the C3 convertase of both the alternative and, more effectively, the classical pathway of complement

activation. VCP may suppress the complement system or their receptor expression, rendering the host less susceptible to the complement-enhancement of HIV infection

- Activation state of a cytokine receptor, e.g., CCR5 receptor or other HIV chemokine coreceptor. For example, poxvirus can interfere with CCR5 activation after HIV binding, e.g., by modulating tyrosine kinase feedback pathways
- One or more of the vaccinia proteins listed in Tables 1 and 2. This includes any poxvirus-encoded protein that specifically interferes with CCR5/CD4/gp120 interactions, including, e.g., vaccinia encoded CC chemokine binding proteins and/or IFN-gamma receptor-like protein
- RNA interference with HIV expression/replication in infected cell
- Alpha-defensins 1, 2, and/or 3
- Soluble factors including those produced by CD8+ lymphocytes and sometimes referred to as CAF
- Interference with the HIV life cycle, including viral entry, import into the host cell nucleus, viral integration into host genome, Rev-dependent and Rev-independent transport from the host nucleus, replication, gene expression, RNA splicing, etc
- Inhibiting HIV replication, including its ability to make copies of itself in the cell, and for productive viral particles to be extruded into the blood
- Inhibiting the ability of HIV to infect a cell, e.g., to bind to CD4 and/or its coreceptor, for the envelope protein to fuse with the host cell membrane, etc.
- Modulating gene expression of the HIV virus, including modulating regulatory genes (e.g., tat and rev), accessory genes (e.g., vif, vpu, vpr, and nef), structural genes (e.g., gag, pol, and env), inner core polypeptides (e.g., gag, p17, p24, p7, and p9), viral enzymes (pol, reverse transcriptase, protease, and integrase), and envelope proteins (e.g., env, gp120, and gp41). The phrase "gene expression" is used broadly to mean any step in the pathway from viral RNA to protein synthesis, and therefore includes all regulatory processes, transcription, translation, polypeptide processing, etc.
- Modulating activity of a HIV encoded polypeptide, including, tat, rev, vif, vpu, vpr, nef, gag, p17, p24, p7, p9, pol, reverse transcriptase, protease, integrase, env, gp120, gp41, etc.

- Modulating viral regulatory sequences, such as RRE, cis-acting repressive sequences (CRS), and inhibitory/instability RNA sequences (INS)

- Any cell or tissue of the immune system, including, but not limited to, lymphocytes, B lymphocytes, T lymphocytes, helper T cells, cytotoxic (or cytolytic) T cells ("CTL), natural killer (NK) cells, naïve T cells, memory T cells, CD4+ helper T cells, CD8+ CTLs, monocytes, macrophages, antigen-presenting cells (APCs), dendritic cells, granulocytes, etc.

The present invention also provides kits comprising a poxvirus. For example, a kit for preventing HIV infection, comprising: an effective amount of a poxvirus, and instructions for administering an effective amount of said poxvirus to a subject to prevent HIV infection; and a kit for treating HIV infection, comprising: an effective amount of a poxvirus, and instructions for administering an effective amount of said poxvirus to a subject to treat HIV infection. The instructions can provide any information that is useful for directing the administration of the poxvirus for the desired purpose.

The present invention also provides methods of advertising, licensing, selling, purchasing, etc., a poxvirus for the purpose of treating and/or preventing HIV infection. Methods can comprise, one or more of the following steps in any effective order: e.g., displaying information (a) comprising instructions for administering a poxvirus for treating and/or preventing HIV infection or (b) comprising a description of the use of poxvirus for treating and/or preventing HIV infection, in a printed or computer-readable medium (e.g., on the Web, Internet, personal computer, server, etc); offering for sale a poxvirus for treating and/or preventing HIV infection in a printed or computer-readable medium; accepting an offer to purchase poxvirus for said use in a printed or computer-readable medium.

EXAMPLES

The following experiments were performed in the laboratory of Dr. Beda Brichacek and Dr. Michael Bukrinsky of the Department of Microbiology and Tropical Medicine, The George Washington University, Washington D.C. 20037.

5

Methods

Subject selection and specimen collection.

Twenty subjects were chosen for inclusion in the study. Ten subjects had been immunized with vaccinia within the previous 3 to 6 months, and ten subjects had never been immunized with vaccinia. All subjects were healthy and had a negative HIV test within the previous year. No subjects of northern European descent were used in order to avoid the potentially complicating factor of including a subject who might be homozygous for the CCR5-delta32 mutation. Two tubes of heparinized blood and 1 serum separator tube were collected. All blood samples from all subjects were drawn within 6 hours of each other, and were immediately processed to separate the PBMCs using standard methods of Ficoll-Hypaque centrifugation.

15

Cell culture preparation.

PBMCs were centrifuged at 1200 rpm for 11 minutes and resuspended in RPMI tissue culture medium + 10% fetal calf serum + 10 µg/ml gentamicin at a concentration of about $1-3 \times 10^6$ cells/ml with a final concentration of 2×10^6 cells/culture. Cell cultures were incubated in a CO₂ incubator. On the second day, one of the utilized strains of HIV was mixed with either culture medium or serum from each individual subject and incubated on ice for 7 hours after which 175 µl of each mixture was added to the autologous cell cultures. The next day 1 ml of cell culture media was added and the cultures were incubated for 5 hours to dilute the viral inoculum and to allow the virus to detach. The supernatant was carefully aspirated and 1 ml of fresh media was added before the cultures were spun down at 1000 rpm for 7 minutes. The supernatant was again aspirated and 2 ml of fresh media was added to each culture. 150 µl of supernatant for RT analysis was aspirated from each culture tube on days 2, 5, 8 and 10, and if needed, up to an additional 1 ml was aspirated and replaced with fresh media. On day 2, PHA was added to the tubes of

25

30

culture series F to act as a cell activator. On day 5, 2 ml of supernatant was removed from each of tubes of culture series F and replaced with 2 ml media + human serum + IL-2.

5 Reverse Transcriptase (RT) analysis.

The measurements of viral replication were performed by standard RT assays using tritiated thymidine as described in numerous articles in the scientific literature. See, e.g., Rey et al., *Virology*, 181(1), 165-71, 1991.

10 Results

All results are based on RT analysis using tritiated thymidine, and are given in counts per minute (CPM).

Culture Series A, the control, demonstrated no viral replication in any cultures.

15 Culture Series B (without serum; Fig. 1A) demonstrated a significant reduction of viral replication in most cultures from vaccinated subjects when compared to unvaccinated subjects. Two subjects (1 and 10) showed a complete lack of viral replication, comparable to the controls in culture series A. One subject was excluded from all analyses when it was subsequently discovered that the subject had
20 had a highly anomalous reaction to the vaccinia immunization with recurrent skin lesions for months afterward. This suggested an inadequate immune response to the vaccinia, and this subject correspondingly did not show any protection against HIV in cell culture, demonstrating viral replication comparable to unvaccinated subjects.

Culture Series C (with serum; Fig. 1B) also demonstrated a significant
25 reduction of viral replication in most cultures from vaccinated subjects, when compared to unvaccinated subjects. The same two subjects (1 and 10) noted in culture series B also had no demonstrable viral replication, comparable to the controls in culture series A. The addition of autologous serum in culture series C further enhanced the difference between vaccinated and unvaccinated subjects when
30 compared to culture series B (no serum).

Culture Series D, E and F, using the T-cell (CXCR4) tropic HIV (Fig. 1C), demonstrated no difference between vaccinated and unvaccinated subjects, including

the two subjects (1 and 10) who were resistant to infection by the macrophage (CCR5) tropic HIV in culture series B and C. As stated in the methods section, care was taken in the selection of subjects to avoid those of northern European descent who might be homozygous for the CCR5-delta32 mutation, so this cannot be an
5 explanation for the described resistance. There was also no difference noted between the addition of serum and no serum (cultures D and E).

Discussion

By at least day 10, there is a statistically significant difference between the
10 vaccinated and non-vaccinated subjects in culture series B and C ($p=.035$ and $.013$ respectively) that increases by day 13 ($p=.017$ and $.008$ respectively), indicating a resistance to infection by HIV in the vaccinated subjects (Fig. 1). Subjects 1 and 10 demonstrated total resistance to macrophage (CCR5) tropic HIV infection in both culture series B and C, with RT measurements equal to the non-HIV infected control
15 (culture series A). The fact that the same result was achieved in both sets of cultures, while infection was easily achieved with the T-cell (CXCR4) tropic HIV in cultures D, E and F, indicate these finding were not the result of laboratory error.

Without further elaboration, it is believed that one skilled in the art can, using the preceding description, utilize the present invention to its fullest extent. The
20 following preferred specific embodiments are, therefore, to be construed as merely illustrative, and not limitative of the remainder of the disclosure in any way whatsoever. The entire disclosure of all applications, patents and publications, cited above and in the figures are hereby incorporated by reference in their entirety, including of U.S. Provisional Application Nos. 60/491,258 filed July 31, 2003,
25 60/493,767 filed August 11, 2003, 60/496,908 filed August 22, 2003, and 60/501,832 filed September 11, 2003.

TABLE 1
THE OPEN READING FRAMES OF VACCINIA VIRUS

Gene ^a	Translation ^b		Size ^c		Characteristics ^d	References
	Start	Stop	aa	M _r		
C23L*	5008	4277	244	26.4	Nonessential; B29R Acidic ^e (4.2)	Perkus, et al. (1990b)
C22L*	6113	5748	122	13.6	Nonessential; B28R Hydrophobic N-terminus	Perkus, et al. (1990b)
C21L*	6815	6477	113	13.4	Nonessential; B27R	Perkus, et al. (1990b)
C20L*	7132	6824	103	12.5	Nonessential; B26R Basic (9.0)	Perkus, et al. (1990b)
C19L*	7856	7080	259	30.5	Nonessential; B25R Hydrophobic N-terminus	Perkus, et al. (1990b)
C18L*	8693	8244	150	17.5	Nonessential; B24R Acidic (4.8)	Perkus, et al. (1990b)
C17L*	9947	8790	386	44.9	Nonessential; B23R	Perkus, et al. (1990b)
C16L*	10539	9997	181	21.0	Nonessential; B22R	Perkus, et al. (1990b)
C15L*	11153	10881	91	10.5	Nonessential; B21R	Perkus, et al. (1990b)
C14L	12212	11967	82	9.3	Nonessential Basic (9.2)	Perkus, et al. (1990b)
C13L	12510	12316	65	7.4	Nonessential Acidic (4.0)	Perkus, et al. (1990b)
C12L	13733	12675	353	40.4	Serine Protease Inhibitor Nonessential	Kotwal and Moss (1988b) Perkus, et al. (1990b)
C11R	14178	14603	142	15.8	Acidic (4.8) Growth Factor Nonessential EGF-like type A domain Hydrophobic C-terminus	Blomquist, et al. (1984); Brown, et al. (1985); Reisner (1985) Buller, et al. (1988); Perkus, et al. (1990b)
C10L	15754	14762	331	38.5	Nonessential Acidic (4.5)	Perkus, et al. (1990b)
C9L	18136	16235	634	74.7	Nonessential	Perkus, et al. (1990b); Kotwal and Moss (1988b)
C8L	18733	18182	184	21.6	Nonessential	Kotwal and Moss (1988b); Perkus, et al. (1990b)
C7L	19257	18808	150	18.0	Acidic (4.4) Nonessential	Kotwal and Moss (1988b); Perkus, et al. (1990a,b)
C6L	19939	19487	151	17.4	Host range function Nonessential	Perkus, et al. (1990a) Kotwal and Moss (1988b); Perkus, et al. (1990b)
CSL	20680	20069	204	24.5	Acidic (4.8) Nonessential	Kotwal and Moss (1988b); Perkus, et al. (1990b)
C4L	21693	20746	316	37.2	Acidic (4.8) Nonessential	Kotwal and Moss (1988b); Perkus, et al. (1990b)
C3L	22551	21763	263	28.6	Nonessential C4B binding protein homolog; virokinase	Kotwal and Moss (1988a,b); Perkus, et al. (1990b)
C2L	24156	22621	512	59.2	Nonessential	Kotwal and Moss (1988a) Kotwal and Moss (1988b); Perkus, et al. (1990b)
C1L	24900	24229	224	26.4	Hydrophobic N-terminus Nonessential Basic (9.0)	Kotwal and Moss (1988b); Perkus, et al. (1990b)

Reprinted from *Virology*, Vol. 179, S. J. Goebel, G. P. Johnson, M. E. Perkus, S. W. Davis, J. P. Winslow and E. Paoletti, "The Complete DNA Sequence of Vaccinia Virus", pgs. 247-266 (1990), with permission from Elsevier.

TABLE 1—Continued

Gene ^a	Translation		Size		Characteristics	References
	Start	Stop ^b	aa	M _r ^c		
N1L	25240	24890	117	14.0	Nonessential Virokine Acidic (4.2)	Kotwal and Moss (1988b); Perkus, et al. (1990b) Kotwal and Moss (1988a)
N2L	25886	25362	175	20.8	Nonessential	Kotwal and Moss (1988a,b); Perkus, et al. (1990b)
M1L	27346	25931	472	54.2	Nonessential Homology to K1L	Perkus, et al. (1990b)
M2L	27986	27327	220	25.1	Nonessential Hydrophobic N-terminus	Perkus, et al. (1990a) Perkus, et al. (1990b)
K1L	28975	28124	284	32.6	Host range function Nonessential	Gillard, et al. (1986); Perkus, et al. (1989) Perkus, et al. (1990b)
K2L	30313	29207	369	42.3	Serine protease inhibitor Nonessential Basic (9.3)	Boursnell, et al. (1988) Perkus, et al. (1990b)
K3L	30629	30366	88	10.5	Nonessential Basic (9.3)	Perkus, et al. (1990b)
K4L	31955	30684	424	48.9	Translation initiation factor Homology to F13L Nonessential	Boursnell, et al. (1988) Perkus, et al. (1990b)
K5L	32497	32090	136	15.2	Nonessential Basic (10.2)	Perkus, et al. (1990b)
K6L	32764	32522	81	9.1	Nonessential	Perkus, et al. (1990b)
K7R	32903	33349	149	17.5	Nonessential Acidic (4.4) Hydrophobic C-terminus	Perkus, et al. (1990b)
F1L	34097	33420	226	26.4	Nonessential Acidic (4.4) Hydrophobic C-terminus	Perkus, et al. (1990b)
F2L	34552	34112	147	16.3	Retroviral protease Nonessential dUTPase	Slabaugh and Roseman (1989) Perkus, et al. (1990b)
F3L	36018	34579	480	55.7	Nonessential	Perkus, et al. (1990b)
F4L	36988	36032	319	37.0	Ribonucleotide reductase (small subunit) Nonessential Acidic (4.6)	Slabaugh, et al. (1988) Perkus, et al. (1990b)
F5L	37985	37023	321	36.5	Multiply hydrophobic	
F6L	38239	38018	74	8.6	Acidic (4.1)	
F7L	38533	38258	92	11.0	- (Lys-Asn) ₉	
F8L	38878	38684	65	7.8	Basic (9.9)	
F9L	39576	38941	212	23.8	Hydrophobic C-terminus	
F10L	40882	39566	439	52.2	Protein kinase 2nd signature	
F11L	41969	40908	354	39.7	-	
F12L	43919	42015	635	73.2	-	
F13L	45079	43964	372	41.8	Envelope antigen	Hirt, et al. (1986)
F14L	45318	45100	73	8.3	Acidic (2.9)	
F15L	46068	45595	159	18.6	Basic (9.5)	
F16L	46770	46078	231	26.6	Basic (9.6)	
F17R	46833	47135	101	11.3	Basic (9.8)	
E1L	48574	47138	479	55.6	-	
E2L	50784	48574	737	85.9	-	
E3L	51483	50914	190	21.5	Acidic (4.9)	
E4L	52318	51542	259	29.8	Acidic (4.9) Transcription factor	

TABLE 1—Continued

Gene ^a	Translation		Size		Characteristics	References
	Start	Stop ^b	aa	M _r ^c		
E5R	52395	53387	331	39.1	(ts: C19??) ^f	Condit, et al. (1983)
E6R	53527	55227	567	66.7	Basic (9.8)	
E7R	55314	55811	166	19.5	-	Earl, et al., 1986
E8R	55939	56757	273	31.9	Basic (9.3)	
E9L	59787	56770	1006	117.0	DNA Polymerase	
					ts: C42, NG26;	
					PAA ^r , Aphidicolin ^r	Traktman, et al. (1989b)
					DNA polymerase family B signature	
E10R	59819	60103	95	10.8	-	
E11L	60490	60104	129	14.9	-	
O1L	62477	60480	666	77.6	Leucine Zipper Motif	
O2L	62851	62528	108	12.4	Glutaredoxin	
I1L	63935	63000	312	35.8	-	Schmitt and Stunnenberg (1988)
I2L	64163	63945	73	8.4	Hydrophobic C-terminus	
					Acidic (3.9)	
					-	
I3L	64973	64167	269	30.0	-	Tengelsen, et al. (1988)
I4L	67371	65059	771	87.0	Ribonucleotide reductase (large subunit)	
					Nonessential	Perkus, et al. (unpublished)
					Divalent Fe-S ferredoxin binding region signature	
I5L	67637	67401	79	8.7	Basic (9.9)	Child, et al., (1990)
I6L	68804	67659	382	43.4	Basic (9.2)	
I7L	70068	68800	423	49.0	-	
I8R	70074	72101	676	77.6	ATP/GTP binding motif A	
G1L	73883	72111	591	67.9	-	
G2R	74209	74868	220	25.7	-	
G3L	74215	73883	111	12.8	Hydrophobic N-terminus	
G4L	75215	74844	124	14.0	Acidic (4.8)	
G5R	75218	76519	434	49.9	Acidic (4.8)	
G6R	76723	77217	165	18.9	-	
G7L	78300	77188	371	41.9	-	
G8R	78331	79110	260	29.9	-	
G9R	79133	80152	340	38.8	Hydrophobic C-terminus	
L1R	80156	80905	250	27.3	Hydrophobic near C-terminus	
L2R	80940	81200	87	10.2	-	
L3L	82245	81196	350	40.6	Multiply hydrophobic	
L4R	82270	83022	251	28.5	Structural protein, VP8	Yang, et al. (1988)
L5R	83035	83418	128	14.0	Basic (10.0)	
J1R	83378	83836	153	17.8	-	
J2R	83855	84385	177	20.1	Thymidine kinase	
					Nonessential	Weir and Moss (1983); Hruby et al. (1983)
					ATP/GTP binding motif A	
J3R	84454	85452	333	15.2	Basic (10.0)	Mackett, et al. (1982)
J4R	85370	85924	185	21.3	RNA Polymerase subunit	
					ts: C7, C20	Broyles and Moss (1986)
					-	
J5L	86403	86005	133	15.2	Hydrophobic C-terminus	Hooda-Dhingra, et al. (1989); Thompson, et al. (1989)
J6R	86510	90367	1286	146.8	RNA Polymerase subunit	
					ts: E8, E13, E72	Broyles and Moss (1986)
					C51, C53, C65	
					-	Ensinger (1987)
					-	
					-	Hooda-Dhingra, et al., (1989); Thompson, et
					-	

TABLE 1—Continued

Gene ^a	Translation		Size		Characteristics	References
	Start	Stop ^b	aa	M _r ^c		
H1L	90882	90370	171	19.7	Basic (9.6)	
H2R	90896	91462	189	21.5	Hydrophobic N-terminus	
H3L	92442	91471	324	37.5	Multiply hydrophobic	
H4L	94830	92446	795	93.6	-	
H5R	95016	95624	203	22.3	-	
H6R	95628	96569	314	36.7	Basic (10.0)	
H7R	96609	97046	146	16.9	DNA topoisomerase	Shuman and Moss (1987)
D1R	97093	99624	844	96.7	mRNA capping enzyme (small subunit)	Morgan, et al. (1984)
D2L	100026	99589	146	16.9	ts: E52, E94	Seto, et al. (1987)
D3R	100019	100729	237	28.0	ts: C5, C35	Seto, et al. (1987)
D4R	100732	101385	218	25.0	-	
D5R	101420	103774	785	90.0	ts: C17, C24, E69	Seto, et al. (1987)
D6R	103818	105728	637	73.8	ATP/GTP binding motif A Early transcription factor subunit	Broyles and Fesler (1990)
D7R	105758	106240	161	17.9	ts: C46, E93 Hydrophobic N-terminus RNA polymerase subunit	Seto, et al. (1987) Ahn, et al. (1990)
D8L	107120	106209	304	35.3	ts: C21, E45 Acidic (4.5) Carbonic anhydrase Transmembrane Cell surface binding Multiply hydrophobic Basic (9.1)	Seto, et al. (1987) Niles, et al. (1986) Niles and Seto (1988) Maa, et al (1990)
D9R	107162	107800	213	25.0	-	
D10R	107800	108543	248	28.9	-	
D11L	110442	108550	631	72.4	NTPase	Rodriguez, et al. (1986); Broyles and Moss (1987)
D12L	111340	110480	287	33.4	ts: C36, C50, E17 Basic (9.0) mRNA capping enzyme (small subunit)	Seto, et al. (1987) Niles, et al. (1989)
D13L	1113026	111374	551	61.9	ts: C33, C43, E101 Rifampicin resistance	Seto, et al. (1987) Tartaglia and Paoletti (1985); Baldick and Moss (1987)
A1L	113502	113053	150	17.0	Acidic (5.0)	
A2L	114197	113526	224	26.3	-	
A3L	116372	114441	644	72.6	-	
A4L	117270	116428	281	30.8	Major core protein P4b	Rosel and Moss (1985)
A5R	117308	117799	164	19.0	Acidic (4.6)	
A6L	118917	117802	372	43.1	Acidic (4.2)	
A7L	121073	118944	710	82.3	-	
A8R	121127	121990	288	33.6	Early transcription factor subunit	Gershon and Moss (1990)
A9L	122285	121989	99	11.1	-	
A10L	124961	122289	891	102.3	-	
A11R	124976	125929	318	36.1	Major core protein P4a Hydrophobic C-terminus	Van Meir and Wittek (1988)
A12L	126512	125937	192	20.5	Acidic (4.7)	
A13L	126748	126539	70	7.7	Basic (10.1)	
A14L	127128	126859	90	10.0	Basic (9.7)	
A15L	127580	127299	94	11.0	-	
A16L	128700	127567	378	43.6	-	
A17L	129314	128706	203	23.0	Hydrophobic C-terminus Hydrophobic center	
A18R	129329	130807	493	56.7	Acidic (4.1) Basic (9.3)	

TABLE 1—Continued

Gene ^a	Translation		Size		Characteristics	References
	Start	Stop ^b	aa	M _r ^c		
A19L	131024	130794	77	8.3	-	
A20R	131377	132654	426	49.2	-	
A21L	131378	131028	117	13.6	Hydrophobic N-terminus	
A22R	132620	133147	176	20.7	Basic (9.9)	
A23R	133170	134315	382	44.6	-	
A24R	134315	137806	1164	133.4	RNA polymerase subunit; ts: C27, C29, C32, C47, C62	Hooda-Dhingra, et al. (1990) Hooda-Dhingra, et al. (1990)
A25L	138011	137817	65	7.5	Leucine Zipper Pattern A-type inclusion protein (cowpox virus)	Funahashi, et al. (1988);
A26L	138948	137983	322	37.3	Acidic (3.3) A-type inclusion protein (cowpox virus)	Funahashi, et al. (1988);
A27L	139330	139001	110	12.6	Basic (9.2)	
A28L	139771	139334	146	16.3	Fusion protein	Rodriguez & Esteban (1987)
A29L	140689	139775	305	35.4	-	
A30L	140885	140655	77	8.7	Basic (9.9)	
A31R	141045	141416	124	14.2	Basic (9.0)	
A32L	142288	141389	300	34.4	Ribonucleoprotein RNA-binding region signature Basic (9.2)	
A33R	142316	142870	185	20.5	ATP/GTP Binding motif A	
A34R	142897	143400	168	19.5	-	
A35R	143447	143974	176	20.0	Basic (10.1)	
A36R	144044	144706	221	25.1	Acidic (4.0)	
A37R	144773	145561	263	29.9	Acidic (4.4)	
A38L	146678	145848	277	31.6	-	
A39R	146695	147903	403	45.7	Multiply hydrophobic	
A40R	147932	148435	168	19.3	-	
A41L	149155	148499	219	25.1	Hydrophobic N-terminus	
A42R	149334	149732	133	15.0	Acidic (4.8)	
A43R	149773	150354	194	22.6	Basic (9.9)	
A44L	151733	150696	346	39.4	Profilin	
A45R	151780	152154	125	13.8	-	
A46R	152147	152788	214	24.7	3 β -Hydroxy-5-ene steroid dehydrogenase	
A47L	153690	152959	244	28.3	Superoxide dismutase	
A48R	153789	154400	204	23.2	-	
A49R	154451	154936	162	18.8	Basic (10.0)	
A50R	154972	156627	552	63.4	Thymidylate kinase ATP/GTP binding motif A	Smith, et al. (1989a)
A51R	156683	157684	334	37.7	Acidic (5.0)	
A52R	157757	158326	190	22.7	Acidic (3.9)	
A53R	158635	158943	103	12.0	DNA Ligase	Colinas, et al. (1990); Smith, et al. (1989a); Kerr and Smith (1989)
A54L	158743	158474	90	10.8	Nonessential	Colinas, et al. (1990)
A55R	159442	161133	564	64.7	Nonessential	Davis, et al. (unpublished)
A56R	161186	162130	315	34.8	Hydrophilic N-terminus	Davis, et al. (unpublished)
A57R	162278	162730	151	17.4	Nonessential	Davis, et al. (unpublished)
					Basic (10.4)	Shida, et al. (1987)
					Nonessential	Shida (1986)
					Nonessential	
					Hemagglutinin	
					Hydrophobic C-terminus	
					Acidic (3.9)	

TABLE 1—Continued

Gene ^a	Translation		Size		Characteristics	References
	Start	Stop ^b	aa	M _r ^c		
B1R	162884	163783	300	34.3	ts: C2, C3, C25 Protein Kinase Basic (9.1)	Traktman, et al. (1989a) Howard and Smith (1989)
B2R	163876	164532	219	24.6	-	
B3R	164571	164942	124	14.4	Acidic (4.7)	
B4R	165603	167276	558	65.3	-	
B5R	167383	168333	317	35.1	Multiply hydrophobic Acidic (4.4) <i>Complement control proteins</i> <i>C3L homologue</i>	
B6R	168432	168950	173	20.1	-	
B7R	168991	169536	182	21.3	Hydrophobic N-terminus	
B8R	169594	170409	272	31.2	Hydrophobic N-terminus	
B9R	170499	170729	77	8.8	-	
B10R	170695	171192	166	18.9	-	
B11R	171267	171530	88	9.9	Acidic (3.6) M(DT) _q DVTNV...	
B12R	171600	172448	283	33.4	Protein Kinase	Howard and Smith (1989)
B13R	172562	172909	116	12.8	Hemorrhage-inducing Serine Protease Inhibitor Nonessential Acidic (4.6)	Pickup, et al. (1986) Kotwal and Moss (1989); Perkus, et al. (1990b)
B14R	172887	173552	222	24.9	Hemorrhage-inducing Serine Protease Inhibitor Nonessential Acidic (4.3)	Pickup, et al. (1986) Kotwal and Moss (1989) Perkus, et al. (1990b)
B15R	173632	174078	149	17.4	Nonessential Acidic (4.5)	Perkus, et al. (1990b)
B16R	174272	175141	290	32.5	Nonessential <i>Kinase-related</i> <i>transforming protein</i>	Perkus, et al. (1990b)
B17L	176212	175193	340	39.5	Nonessential	Perkus, et al. (1990b)
B18R	176349	178070	574	68.1	Nonessential	Perkus, et al. (1990b)
B19R	178145	179203	353	40.9	Hydrophobic N-terminus Nonessential	Perkus, et al. (1990b)
B20R	179300	179680	127	15.5	Nonessential Acidic (4.1)	Perkus, et al. (1990b)
B21R*	180585	180857	91	10.5	Nonessential; C15L	Perkus, et al. (1990b)
B22R*	181199	181741	181	21.0	Nonessential; C16L	Perkus, et al. (1990b)
B23R*	181791	182948	386	44.9	Nonessential; C17L	Perkus, et al. (1990b)
B24R*	183045	183494	150	17.5	Nonessential; C18L Acidic (4.8)	Perkus, et al. (1990b)
B25R*	183882	184658	259	30.5	Hydrophobic N-terminus Nonessential; C19L	Perkus, et al. (1990b)
B26R*	184606	184914	103	12.5	Nonessential; C20L Basic (9.0)	Perkus, et al. (1990b)
B27R*	184923	185261	113	13.4	Nonessential; C21L	Perkus, et al. (1990b)
B28R*	185625	185990	122	13.6	Nonessential; C22L Hydrophobic N-terminus	Perkus, et al. (1990b)
B29R*	186730	187461	244	26.4	Nonessential; C23L Acidic (4.2)	Perkus, et al. (1990b)

^a Open reading frames enumerated as described in text.^b Translation stop does not include the three bases of termination codon.^c M_r values calculated for the nascent, unprocessed polypeptide chain are presented as kDa.^d Functions or activities indicated in bold type are known functions of vaccinia virus. Those indicated in *italics* have been identified in this study on the basis of similarity to existing proteins. All others are possible functions previously described by other investigators.^e Acidic proteins: pI < 5.0; basic proteins: pI > 9.0. pI presented within parentheses.^f Temperature-sensitive mutants indicated by ts. Those first isolated by Condit *et al.* (1983) are prefaced with C; 1 begin with E. Mutant C19, while not localized to a particular open reading frame, appears to map in the vicinity of 1^g Open reading frames repeated in both left and right termini of genome.

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ORF ^a	START STOP	AA ^b kDa ^c	name / (putative) function / homologies ^d	BLAST ^e expect	BLAST ^e AA id	HSS ^f (%)	references
001L/ 193R ^a C23L	6822 6412	136 14.9	35k major secr. protein chemokine receptor (f) VAC (C23L/B29R)	6.0e-57	41/42	97	(Patel et al., 1990)
		244	VAR-P G3R	8.9e-51	46/49	93	(Graham et al., 1997)
		253	CPXORFB	5.6e-49	40/42	95	(Goebel et al., 1990)
		258	SFV T1 protein	2.5e-20	23/42	54	(Hu et al., 1994)
		260	Myxoma virus T1/35kDa	1.5e-14	21/42	50	(Upton et al., 1987)
							(Graham et al., 1997)
002L/ 192R ^a	7784 7254	176 19.7	secr. TNF receptor (f) CPX crnB	5.1e-71	76/83	91	(Upton et al., 1991a)
		348	VAR-BSH G2R	1.0e-66	73/83	87	(Hu et al., 1994)
		326	Myxoma virus T2	4.9e-30	21/37	56	(Shchelkunov et al., 1995)
		325	Rabbit fibroin Virus T2	1.8e-28	17/36	47	(Upton et al., 1991a)
		202	CPXC4L	8.7e-15	30/51	58	(Upton et al., 1987)
		346	HS TNF receptor protein	1.9e-08	14/26	53	(Safronov et al., 1996)
C19L		259	VAC (C19L/B25R)	0.00026	16/19	84	(Heiler et al., 1990)
		277	human CD40L receptor	0.0015	11/24	45	(Goebel et al., 1990)
			30 matches to TNF receptors and surface proteins	<0.39			(Stamenovic et al., 1989)
003L/ 191R ^a C17L 004L/ 190R ^a C17L D1L	8780 8472 9558 8857	102 26.9	45k ank ⁺ -like protein (f1) VAC C17L/B23R 45k ank-like protein (f2) VAC (C17L/B23R)	1.3e-39	62/63	98	(Goebel et al., 1990)
		386	VAR-BSH	6.2e-159	110/110	100	(Goebel et al., 1990)
		91	CPX host range	9.1e-31	46/49	93	(Shchelkunov et al., 1995)
		669	VAR-I D6L (BSH:D8L)	1.1e-13	22/50	44	(Spehner et al., 1988)
		452	VAR-I B19R (BSH: B16R)	1.7e-11	21/50	42	(Shchelkunov et al., 1995)
		574	VAC B18R (WR: B17R)	1.2e-05	22/73	30	(Shchelkunov et al., 1995)
		574	VAC C9L	8.6e-05	22/73	30	(Goebel et al., 1990)
		634	VAR-I G1R	0.00011	11/24	45	(Kotwal and Moss, 1988a)
		585	orf virus	0.00013	22/74	29	(Shchelkunov et al., 1995)
		516	VAR-I D7L (BSH:D10L)	0.0088	15/49	30	(Sullivan et al., 1995b)
		153		0.014	12/28	42	(Shchelkunov et al., 1995)
005R C11R D2R	10203 10625	140 15.5	Growth factor (EGF receptor binding) VAC VAR-I (BSH:D4R)	2.9e-82	99/104	95	(Twardzik et al., 1985)
		142	CPX D5R	3.6e-74	106/140	75	(Stroobant et al., 1985)
		140	human epiregulin	3.4e-95	101/114	88	(Goebel et al., 1990)
		138	100 matches to growth factor like sequences	2.2e-14	29/78	37	(Shchelkunov et al., 1995)
		169		<0.10			(Safronov et al., 1996)
							D30783
006L C10L D5L	11758 10778	326 37.9	37.9k protein VAC CPX D6L VAR-BSH (I: D3L) VAR-I D11L (BSH:D14L)	1.7e-235	264/268	98	(Venkatesan et al., 1982)
		331	VAC C4L	7.7e-235	264/268	98	(Goebel et al., 1990)
		330	CPX D16L	3.6e-233	169/171	97	(Safronov et al., 1996)
		316	VAR-I B6R (BSH:BSR)	1.7e-94	34/68	44	(Shchelkunov et al., 1995)
		316	CPX D16L	1.8e-92	30/68	54	(Shchelkunov et al., 1995)
		315	Ectromelia 42K protein	2.3e-92	31/68	45	(Goebel et al., 1990)
		82	FPV BamHI ORF1	1.2e-50	78/82	95	(Safronov et al., 1996)
		418		3.0e-11	13/41	31	(Senkevich et al., 1993a)
007R D4R	12263 12538	91 10.6	28k virulence factor (f) CPX D7R VAC-WR 21.7k protein VAR-I (BSH:D6R)	1.5e-51	42/47	89	(Tomley et al., 1988)
		242	Ectromelia 28k secreted virulence factor	5.3e-51	41/47	87	(Senkevich et al., 1993a)
		184		3.7e-50	41/47	87	(Safronov et al., 1996)
		242		3.7e-50	41/47	87	(Kotwal and Moss, 1988a)
		241					(Shchelkunov et al., 1995)
							(Senkevich et al., 1993a)
008L D7L	13414 13052	120 13.7					

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GENOMIC SEQUENCE OF THE MVA STRAIN

ORF ^a	START STOP	AA ^b	kDa ^c	name / (putative) function / homologues ^d	BLAST ^e expect	BLAST ^e AA id	HSS ^f (%)	references
left	terminal	region:						
D6L	14911	452		VAR-I (BSH: D8L)	2.2e-52	80/85	94	(Shchelkunov <i>et al.</i> , 1995)
		669		CPX host range gene	8.1e-51	77/85	90	(Spehner <i>et al.</i> , 1988)
		153		VAR-I D7L (BSH: D10L)	2.9e-17	19/45	42	(Shchelkunov <i>et al.</i> , 1995)
		634		VACC9L	1.3e-13	19/45	42	(Goebel <i>et al.</i> , 1990)
		1161		C. botulinum NTNH protein	0.00019	6/12	50	(Hutson <i>et al.</i> , 1996)
		202		Capripox	0.00058	15/58	25	(Cao <i>et al.</i> , 1995)
		395		UDP glucose dehydrogenase	0.00051	6/19	31	(Bult <i>et al.</i> , 1996)
		516		orf virus ank-like	0.0064	16/49	32	(Sullivan <i>et al.</i> , 1995b)
		673		rabbit fibroma 77.2k protein	0.0072	12/30	40	(Massung <i>et al.</i> , 1992)
013L	15420	71	8.5	77k CPX hr protein (f5)				(Spehner <i>et al.</i> , 1988)
D6L	15205	669		CPX host range gene	5.2e-44	68/69	98	(Safronov <i>et al.</i> , 1996)
		452		VAR (BSH: D8L)	7.9e-42	64/67	95	(Shchelkunov <i>et al.</i> , 1995)
		673		rabbit fibroma 77.2k protein	0.0052	8/26	30	(Massung <i>et al.</i> , 1992)
		386		VAC C17L/B23R	0.018	14/33	42	(Goebel <i>et al.</i> , 1990)
		202		Capripox	0.023	10/19	52	(Sullivan <i>et al.</i> , 1995b)
		574		VAC B18R (WR: B17R)	0.71	12/28	42	(Goebel <i>et al.</i> , 1990)
		574		VAR B19R (BSH: B16R)	0.71	12/28	42	(Shchelkunov <i>et al.</i> , 1995)
014L	16205	109	13.1	75k ank-like gene (f1)				(Kotwal and Moss, 1988a)
C9L	15876	634		VAC	3.9e-73	109/109	100	(Goebel <i>et al.</i> , 1990)
		614		CPX D11L	1.6e-70	105/108	97	(Safronov <i>et al.</i> , 1996)
D9L		91		VAR (I: D6.5L)	1.2e-52	78/91	85	(Shchelkunov <i>et al.</i> , 1995)
		437		CPX D1L	3.7e-19	28/67	41	(Safronov <i>et al.</i> , 1996)
015L	16786	96	11.2	rabbit fibroma 77.2K protein	0.021	5/16	31	(Massung <i>et al.</i> , 1992)
C9L	16496	634		75k ank-like gene (f2)				(Kotwal and Moss, 1988a)
		614		VAC	4.0e-53	80/80	100	(Goebel <i>et al.</i> , 1990)
		437		CPX D11L	3.9e-25	48/80	60	(Safronov <i>et al.</i> , 1996)
		172		CPX D1L	9.6e-12	14/36	38	(Safronov <i>et al.</i> , 1996)
		141		VAR-Garcia 1966 B11L	0.0001	17/17	100	(Massung <i>et al.</i> , 1996)
		669		integrase (simian foamy v.)	0.033	10/24	41	(Schweizer and Neumann, 1995)
016L	17759	297	35.0	CPX host range gene	0.043	9/17	52	(Spehner <i>et al.</i> , 1988)
C9L	16866	634		75k ank-like gene (f3)				(Kotwal and Moss, 1988a)
		614		VAC	3.4e-208	291/294	98	(Goebel <i>et al.</i> , 1990)
		153		CPX D11L	1.4e-130	90/126	71	(Safronov <i>et al.</i> , 1996)
D7L		669		VAR-I (BSH: D10L)	8.4e-68	84/109	77	(Shchelkunov <i>et al.</i> , 1995)
		452		CPX host range gene	4.5e-17	24/61	39	(Spehner <i>et al.</i> , 1988)
D8L		668		CPX D9L	2.2e-16	23/61	37	(Safronov <i>et al.</i> , 1996)
		386		VAR-BSH (I: D6L)	3.3e-16	21/61	34	(Shchelkunov <i>et al.</i> , 1995)
		833		VAC C17L/B23R	2.9e-08	11/24	45	(Goebel <i>et al.</i> , 1990)
		574		CPX D3L	0.0085	13/58	22	(Safronov <i>et al.</i> , 1996)
		202		VAC B18R (WR: B17R)	0.012	13/40	32	(Goebel <i>et al.</i> , 1990)
		574		Capripox virus	0.084	11/29	37	(Sullivan <i>et al.</i> , 1995b)
				VAR-I B19R (BSH: B16R)	0.090	13/40	32	(Shchelkunov <i>et al.</i> , 1995)
017L	18335	177	20.8	20.8k protein				(Kotwal and Moss, 1988a)
CSL	17802	184		VAC	1.2e-125	125/129	96	(Goebel <i>et al.</i> , 1990)
		182		CPX D12L	5.0e-118	119/126	94	(Safronov <i>et al.</i> , 1996)
		182		VAC B7R	8.3e-06	16/67	23	(Goebel <i>et al.</i> , 1990)
		795		VAC H4L (RAP94)	0.60	12/45	26	(Goebel <i>et al.</i> , 1990)
018L	18859	150	18.0	host range protein				(Perkus <i>et al.</i> , 1991)
C7L	18407	150		VAC	1.6e-106	150/150	100	(Kotwal and Moss, 1988a)
D11L		150		VAR-BSH (I: D8L)	4.2e-106	149/150	99	(Shchelkunov <i>et al.</i> , 1995)
		185		Swinepox virus ORF SwF8a	3.4e-35	31/82	37	(Schnitzlein and Tripathy, 1991)
		197		Capripox virus ORF CF8a	1.4e-31	29/87	33	(Gershon and Black, 1989a)
		170		CPX D4L	3.5e-17	19/60	31	(Safronov <i>et al.</i> , 1996)
		158		Myxoma virus ORF MF8	5.6e-13	16/43	37	(Jackson and Bults, 1992)
		128		VAR-BSH D3L (I: D1.5L)	5.4e-06	18/60	30	(Shchelkunov <i>et al.</i> , 1995)
019L	19541	157	18.2	18.2k protein				(Kotwal and Moss, 1988a)
C6L	19068	151		VAC	7.6e-104	151/151	100	(Goebel <i>et al.</i> , 1990)
D9L		156		VAR (BSH: D12L)	1.6e-99	145/150	96	(Shchelkunov <i>et al.</i> , 1995)
		156		CPX D14L	1.3e-96	141/150	94	(Safronov <i>et al.</i> , 1996)
		159		Capripox virus ORF T3a	4.4e-07	24/76	31	(Gershon and Black, 1989a)
		151		Rabbit fibroma virus T3Aa	0.0047	16/46	34	(Upton <i>et al.</i> , 1987)
		181		VAC C16L/B22R	0.2	12/46	26	(Goebel <i>et al.</i> , 1990)
		149		VAR C4R	0.29	8/13	61	(Shchelkunov <i>et al.</i> , 1995)
		149		VAC-WR K7R	0.40	8/13	61	(Kotwal and Moss, 1988a)
020L	20025	113	13.2	14k virulence factor, secreted protein (f)				(Kotwal and Moss, 1988a)
N1L	19684	117		VAC	2.6e-60	92/102	90	(Kotwal and Moss, 1988b)
		117		CPX P1L	7.3e-58	85/102	83	(Goebel <i>et al.</i> , 1990)
P1L		117		VAR-BSH, virokinase	6.6e-56	88/102	86	(Shchelkunov <i>et al.</i> , 1995)
		107		Rabbit fibroma virus	0.015	10/17	58	(Safronov <i>et al.</i> , 1996)
								(Massung <i>et al.</i> , 1992)
021L	20656	170	20.3	alpha-amanitin sensitive protein				(Tamin <i>et al.</i> , 1991)
N2L	20144	175		CPX P2L	3.0e-118	138/142	97	(Kotwal and Moss, 1988a)
P2L		175		VAC	6.1e-118	137/142	96	(Safronov <i>et al.</i> , 1996)
		177		VAR	9.7e-115	135/142	95	(Goebel <i>et al.</i> , 1990)
								(Shchelkunov <i>et al.</i> , 1995)
022L	20981	98	11.0	33k host range gene (f)				(Gillard <i>et al.</i> , 1986)
K1L	20685	284		VAC	1.8e-56	86/88	97	(Altenburger <i>et al.</i> , 1989)
		284		CPX M1L	2.3e-56	86/88	97	(Safronov <i>et al.</i> , 1996)
C1L		66		VAR	2.0e-39	63/66	95	(Shchelkunov <i>et al.</i> , 1995)
		65		human NOTCH 2	0.00036	17/41	41	(Kuisanis <i>et al.</i> , 1996)

ORF*	START STOP	AA ^b	kDa ^c	name / (putative) function / homologies ^d	BLAST ^e expect	BLAST ^e AA id	HSS ^f (%)	references
	left	terminal	region:					
023L	22296 21187	369	42.3	serpin SPI-3, cell-cell fusion mutation				(Boursnell <i>et al.</i> , 1988)
K2L		369		VAC	1.2e-258	365/369	98	(Altenburger <i>et al.</i> , 1989)
C2L		373		CPX M2L	1.2e-256	331/337		(Goebel <i>et al.</i> , 1990)
		373		VAR-BSH	9.9e-249	321/337	95	(Safronov <i>et al.</i> , 1996)
		373		Ectromelia virus H14-B	6.5e-244	312/337		(Shchelkunov <i>et al.</i> , 1995)
		386		HS plasminogen activator inhibitor 1	1.1e-35	30/68	44	U67964 (Loskutov <i>et al.</i> , 1987)
		58		CPX SPI 3 protein	8.2e-33	57/58	98	gi:1168082
		369		Myxoma virus MAPI gene	7.3e-32	33/131	25	(Upton <i>et al.</i> , 1990a)
		397		mouse protease nexin	1.5e-29	31/67	46	(Vassalli <i>et al.</i> , 1993)
		397		humane glia derived neurite- promoting factor	8.7e-27	30/65	46	A03911
		320		Swinepox SPI like protein	3.6e-21	20/70	28	(Massung <i>et al.</i> , 1993)
		417		a-1 antitrypsin, human	2.2e-20	26/66	39	(Ciliberto <i>et al.</i> , 1985)
		383		Corticosteroid-binding protein (rabbit)	9.0e-20			(Seralini <i>et al.</i> , 1989)
		390		squamous cell carcinoma antigen	1.9e-17			(Schneider <i>et al.</i> , 1995)
024L	22612 22346	88	10.5	IFN resistance, eIF-2a homolog				(Beattie <i>et al.</i> , 1991)
		88		CPX M3L	2.6e-61	88/88	100	(Davies <i>et al.</i> , 1992)
K3L		88		VAC	1.4e-60	87/88	98	(Safronov <i>et al.</i> , 1996)
C3L		88		VAR-1	1.0e-52	73/88	82	(Goebel <i>et al.</i> , 1990)
		86		SPV C8 protein translation initiation factor 2 family	4.1e-22 1.2e-08/ 0.45	20/44	45	(Shchelkunov <i>et al.</i> , 1995) (Massung <i>et al.</i> , 1993)
025L	23938 22664	424	48.9	phospholipase D-like protein				(Cao <i>et al.</i> , 1997)
K4L		424		VAC	1.5e-306	423/424	99	(Goebel <i>et al.</i> , 1990)
		424		CPX M4L	2.1e-303	416/424	98	(Safronov <i>et al.</i> , 1996)
		437		human HU-K4	2.8e-135	53/95	55	U60644
		372		D. discoideum	2.5e-91	28/47	59	(Giorda <i>et al.</i> , 1989)
		516		C. elegans	6.6e-89	31/61	50	gi: 2435624
		2327		C. elegans	2.8e-52	36/60	60	gi: 2291241
		635		C. elegans	1.1e-24	19/53	35	(Wilson <i>et al.</i> , 1994)
		377		FPV major envelope protein	2.9e-23	19/61	31	(Calvert <i>et al.</i> , 1992)
		371		Myxoma virus env protein	3.6e-22	18/51	35	U43549
		378		Orf virus env protein 82L	1.2e-21	21/71	29	(Sullivan <i>et al.</i> , 1994)
MC021L		388		MCV subtype 1 env protein	3.2e-21	20/63	31	(Senkevich <i>et al.</i> , 1997)
C17L		372		VAR-BSH	4.6e-19	15/52	28	(Shchelkunov <i>et al.</i> , 1995)
		372		VAC F13L	4.9e-17	15/52	28	(Goebel <i>et al.</i> , 1990)
026L	24478 23966	170	19.1	lysophospholipase-like protein (f1)				(Upton & Buller, unpub.)
		276		CPX M5L	2.6e-110	161/170	94	(Safronov <i>et al.</i> , 1996)
K5L		277		Ectromelia virus H14-E	2.7e-109	160/170	94	X94355 U67964
		136		VAC	5.5e-69	107/108	99	(Goebel <i>et al.</i> , 1990)
		134		VAC-WR	8.3e-63	98/101	97	(Boursnell <i>et al.</i> , 1988)
		313		HS lysophospholipase	3.3e-35	35/105	33	U67963
		323		homolog	1.2e-13	30/94	31	Z97050
		324		poss. oxidoreductase M. tuberculosis	3.1e-5	13/58	22	U95973
		313		Lysophospholipase isolog A. thaliana	0.047	13/30	43	U32747
				H. influenza probable lysophospholipase L2				
027L	24694 24500	64	7.0	lysophospholipase-like protein (f2)				(Upton & Buller, unpub.)
K6L		81		VAC	5.3e-42	63/63	100	(Boursnell <i>et al.</i> , 1988)
		276		CPX M5L	2.4e-36	57/58	98	(Safronov <i>et al.</i> , 1996)
		277		Ectromelia virus H14-E	2.4e-36	57/58	98	U67964
		313		HS lysophospholipase homolog	9.1e-23	34/53	64	U67963
		323		hyp. oxidoreductase M. tuberculosis	9.9e-14	22/54	40	Z97050
		530		dihydrotestosterone/androsta- nediol UDP-glucuronosyl- transferase	7.0e-05	6/17	35	A48633
	central	conserved	region:					
028R	24864	149	17.5	17.5k protein				(Goebel <i>et al.</i> , 1990)
K7R	25313	149		VAC	6.1e-105	149/149	100	(Goebel <i>et al.</i> , 1990)
		161		CPX M6R	1.6e-101	144/149	96	(Safronov <i>et al.</i> , 1996)
C4R		149		VAR	4.9e-101	143/149	100	(Shchelkunov <i>et al.</i> , 1995)
		236		Swinepox (sc76)	0.00017	19/49	95	(Massung <i>et al.</i> , 1993)
029L	26046	222	25.9	25.9k protein				(Roseman and Slabaugh, 1990)
F1L	25378	226		VAC	2.7e-158	208/211	98	(Goebel <i>et al.</i> , 1990)
		238		CPX G1L	7.0e-148	166/189	87	(Safronov <i>et al.</i> , 1996)
C5L		251		VAR-1	6.6e-147	184/200	92	(Shchelkunov <i>et al.</i> , 1995)
030L	26501 26058	147	16.2	dUTPase				(Roseman and Slabaugh, 1990)
F2L		147		VAC	2.9e-102	147/147	100	(Roseman <i>et al.</i> , 1996)
		147		CPX G2L	8.2e-100	144/147	97	(Goebel <i>et al.</i> , 1990)
		147		VAR	1.1e-97	142/147	96	(Safronov <i>et al.</i> , 1996)
C6L		164		human dUTPase	4.1e-61	49/69	71	(Shchelkunov <i>et al.</i> , 1995) (Ladner <i>et al.</i> , 1996)

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF ^a	START STOP	AA ^b	kDa ^c	name / function	(putative) / homologues ^d	BLAST ^e expect	BLAST ^e AA id	HSS ^f (%)	references
left terminal region:									
	142			Swinepox virus		8.0e-56	43/70	61	(Massung <i>et al.</i> , 1993)
	159			orf virus		1.5e-49	45/69	65	(Mercer <i>et al.</i> , 1989)
	178			avian adenovirus		6.6e-49	40/70	57	(Akopian <i>et al.</i> , 1992)
	1124			FIV pol polyprotein		1.5e-26	49/117	41	(Talbot <i>et al.</i> , 1989)
				dUTPase pyrophosphatase family		>4.2e-06			
031L	27955	476	55.3	kelch-like protein					(Senkevich <i>et al.</i> , 1993b)
	26525								(Roseman and Slabaugh, 1990)
F3L		480		VAC		0.0	292/294	99	(Goebel <i>et al.</i> , 1990)
		485		CPX G3L		0.0	287/293	97	(Safronov <i>et al.</i> , 1996)
C7L		179		VAR-I		1.9e-124	166/179	92	(Shchelkunov <i>et al.</i> , 1995)
		500		Swinepox virus protein C13		4.4e-46	39/133	29	(Massung <i>et al.</i> , 1993)
		564		VAC A5SR		2.8e-21	17/51	33	(Goebel <i>et al.</i> , 1990)
		689		kelch protein D.melanogaster		5.3e-18	21/65	32	(Xue and Cooley, 1993)
		512		CPX D18L		1.4e-16	15/33	45	(Safronov <i>et al.</i> , 1996)
		512		VAC C2L		1.6e-16	15/33	45	(Goebel <i>et al.</i> , 1990)
		625		T27E9.4 C. elegans		3.7e-14	15/59	25	Z82059
		624		human KIAA0132 protein		1.9e-13	13/60	21	D50922 o.k.
		817		R09A8.3 (C. elegans)		1.1e-12	17/45	37	(Wilson <i>et al.</i> , 1994)
		611		C47D12.7 (C. elegans)		2.4e-12	22/91	24	(Wilson <i>et al.</i> , 1994)
		530		Swinepox virus		3.0e-09	14/58	24	(Massung <i>et al.</i> , 1993)
		589		MM ^m actin binding protein		1.9e-09	18/88	20	U65079
		521		CPX C3L		1.2e-08	15/37	40	(Safronov <i>et al.</i> , 1996)
		509		Myxoma virus MT-9		2.5e-08	17/58	29	(Upton <i>et al.</i> , 1990a)
		202		Murine IAP-promoted placenta (MIPP) expressed protein		4.3e-08	17/56	30	(Chang-Yeh <i>et al.</i> , 1991)
		326		A. thaliana hyp. protein		3.9e-06	22/80	27	Z99708
		559		Ectromelia virus p65		9.0e-6	12/31	38	(Senkevich <i>et al.</i> , 1993b)
		916		β-scrutin (L. polyphemus)		0.00016	13/42	30	(Way <i>et al.</i> , 1995)
		172		VAR-I J8R (BSH: I6R)		0.018	15/36	41	(Shchelkunov <i>et al.</i> , 1995)
032L	28925	319	37.0	ribonucleotide reductase (small subunit)					(Slabaugh <i>et al.</i> , 1988)
	27966								(Roseman and Slabaugh, 1990)
		319		CPX G4L		2.3e-231	317/319	99	(Safronov <i>et al.</i> , 1996)
F4L		319		VAC		3.5e-231	317/319	99	(Goebel <i>et al.</i> , 1990)
C8L		333		VAR-BSH		4.1e-228	313/319	98	(Shchelkunov <i>et al.</i> , 1995)
				ribonucleotide reductase family		>2.2e-10			
033L	29250	97	11.1	36.5k major membrane protein precursor (f1)					(Roseman and Slabaugh, 1990)
	28957								
C9L		348		VAR-BSH		1.9e-36	51/53	96	(Shchelkunov <i>et al.</i> , 1995)
		323		CPX G5L		2.4e-19	47/77	61	(Safronov <i>et al.</i> , 1996)
F5L		321		VAC		3.3e-19	42/70	60	(Goebel <i>et al.</i> , 1990)
		1584		non-receptor tyrosin kinase (Dictyostelium discoideum)		0.00038	15/35	42	(Tan and Spudich, 1990)
034L	29875	218	24.8	36.5k major membrane protein precursor (f2)					(Roseman and Slabaugh, 1990)
	29219								
		323		CPX G5L		8.2e-155	215/217	99	(Safronov <i>et al.</i> , 1996)
F5L		321		VAC		6.4e-155	215/217	99	(Goebel <i>et al.</i> , 1990)
C9L		348		VAR-BSH		6.8e-141	186/210	88	(Shchelkunov <i>et al.</i> , 1995)
035L	30129	74	8.6	8.6k protein					(Roseman and Slabaugh, 1990)
F6L	29905	74		VAC		5.5e-47	74/74	100	(Goebel <i>et al.</i> , 1990)
C10L		72		VAR		2.3e-38	62/70	88	(Shchelkunov <i>et al.</i> , 1995)
036L	30387	80	9.4	9.4k protein					(Roseman and Slabaugh, 1990)
C11L	30145	79		VAR		2.9e-44	34/43	79	(Shchelkunov <i>et al.</i> , 1995)
F7L		92		VAC		1.9e-43	65/65	100	(Goebel <i>et al.</i> , 1990)
037L	30731	65	7.9	7.9k protein					(Roseman and Slabaugh, 1990)
F8L	30534	65		VAC		5.1e-43	63/65	96	(Goebel <i>et al.</i> , 1990)
C12L		65		VAR-I		3.1e-41	61/65	93	(Shchelkunov <i>et al.</i> , 1995)
038L	31429	212	23.8	23.8k protein					(Roseman and Slabaugh, 1990)
	30791								
		212		VAC		7.1e-148	212/212	100	(Goebel <i>et al.</i> , 1990)
		212		VAR		1.2e-144	207/212	97	(Shchelkunov <i>et al.</i> , 1995)
		215		Swinepox virus		8.1e-72	39/93	41	(Massung <i>et al.</i> , 1993)
MC016L		213		MCV subtype I		2.8e-62	71/152	46	(Senkevich <i>et al.</i> , 1996)
		225		Orf virus		5.1e-39	27/84	32	(Mercer <i>et al.</i> , 1995)
		243		FPV protein FP2		2.8e-17	26/58	44	(Binns <i>et al.</i> , 1988)
		243		MCV subtype I MC069R		7.7e-12	23/58	39	(Senkevich <i>et al.</i> , 1996)
		250		VAC LIR		1.1e-07	20/58	34	(Goebel <i>et al.</i> , 1990)
		250		VAR MIR		1.1e-07	20/58	34	(Shchelkunov <i>et al.</i> , 1995)
039L	32735	439	52.1	serine/threonine kinase 2					(Lin and Broyles, 1994)
	31416								(Wang and Shuman, 1995)
		439		VAC		0.0	429/439	97	(Goebel <i>et al.</i> , 1990)
F10L		439		VAR-BSH		0.0	424/439	96	(Shchelkunov <i>et al.</i> , 1995)
C14L		440		Swinepox virus		2.2e-233	151/214	70	(Massung <i>et al.</i> , 1993)
MC017L		443		MCV subtype I		2.3e-198	178/282	63	(Senkevich <i>et al.</i> , 1996)
		498		orf virus		2.2e-162	198/366	54	(Mercer <i>et al.</i> , 1995)
040L	33012	84	9.6	39.7k protein (f1)					(Shchelkunov <i>et al.</i> , 1995)
C15L	32758	354		VAR		6.6e-27	50/64	78	(Goebel <i>et al.</i> , 1990)
F11L		354		VAC		9.1e-27	50/64	78	
041L	33771	100	11.4	39.7k protein (f2)					

ORF ^a	START STOP	AA ^b	kDa ^c	name / (putative) function / homologies ^d	BLAST ^e expect	BLAST ^e AA id	HSS ^f (%)	references
	left terminal	region:						
F11L	33469	354		VAC	3.8e-62	95/95	100	(Goebel <i>et al.</i> , 1990).
C15L		354		VAR	8.8e-58	90/95	94	(Shchelkunov <i>et al.</i> , 1995)
042L	35721	635	73.1	73.1k protein				
F12L	33814	635		VAC	0.0	629/635	99	(Goebel <i>et al.</i> , 1990).
C16L		635		VAR-I	0.0	607/635	95	(Shchelkunov <i>et al.</i> , 1995)
MC019L		352		Myxoma virus	3.6e-84	28/66	42	U43549
		663		MCV subtype I	4.0e-60	29/82	35	(Senkevich <i>et al.</i> , 1996)
		640		orf virus	4.8e-39	19/61	31	U34774
		630		FPV F12 homolog	2.3e-15	19/67	28	(Ogawa <i>et al.</i> , 1993)
043L	36866 35748	372	41.8	37k major EEV antigen IMCBH sensitive protein palmitoylprotein				(Hirt <i>et al.</i> , 1986) (Schmutz <i>et al.</i> , 1991) (Grosenbach <i>et al.</i> , 1997)
F13L		372		VAC	2.1e-268	369/372	99	(Goebel <i>et al.</i> , 1990)
C17L		372		VAR-BSH	8.9e-265	364/372	97	(Shchelkunov <i>et al.</i> , 1995)
		371		Myxoma virus	2.5e-115	110/200	55	U43549
MC021L		378		orf virus	7.6e-108	83/194	42	(Sullivan <i>et al.</i> , 1994)
		388		MCV subtype I	6.1e-98	44/113	38	(Senkevich <i>et al.</i> , 1996)
		377		FPV major env protein	2.8e-88	47/112	41	(Calvert <i>et al.</i> , 1992)
		251		pigeonpox virus	1.8e-62	47/112	41	S27933
		424		CPX M4L	2.1e-18	16/52	30	(Safronov <i>et al.</i> , 1996)
		424		VAC K4L	1.7e-17	14/35	40	(Goebel <i>et al.</i> , 1990)
		372		D. discoideum	1.4e-16	28/84	33	(Giorda <i>et al.</i> , 1989)
		437		HU-K4 (homo sapiens)	1.5e-11	25/94	26	U60644
044L	37105	73	8.3	8.3k protein				
F14L	36884	73		VAC	2.3e-44	72/73	98	(Goebel <i>et al.</i> , 1990)
C18L		73		VAR	2.1e-35	57/73	78	(Shchelkunov <i>et al.</i> , 1995)
045L	378533	158	18.6	18.6k protein				
F15L	37377	158		VAC	2.3e-112	157/158	99	(Goebel <i>et al.</i> , 1990).
C19L		161		VAR	1.4e-107	150/153	98	(Shchelkunov <i>et al.</i> , 1995)
MC025L		148		MCV subtype I	3.5e-54	52/113	46	(Senkevich <i>et al.</i> , 1996)
		148		Myxoma virus	5.4e-50	48/112	42	U43549
046L	38555	231	26.5	26.5k protein				
F16L	37860	231		VAC	3.3e-159	227/231	98	(Goebel <i>et al.</i> , 1990).
C20L		231		VAR	5.6e-157	222/231	96	(Shchelkunov <i>et al.</i> , 1995)
MC029L		209		Myxoma virus	8.3e-48	26/58	44	U43549
		230		MCV subtype I	6.9e-45	16/61	26	(Senkevich <i>et al.</i> , 1996)
047R	38619 38924	101	11.3	11k DNA binding phosphoprotein				(Bertholet <i>et al.</i> , 1985) (Kao and Bauer, 1987)
F17R		101		VAC	3.0e-69	100/101	99	(Goebel <i>et al.</i> , 1990)
C21R		101		VAR	9.7e-67	99/101	98	(Shchelkunov <i>et al.</i> , 1995)
		102		MYX	6.6e-26	45/92	98	U43549
MC030R		92		MCV subtype I	1.5e-20	33/53	48	(Senkevich <i>et al.</i> , 1997)
		46		orf virus	1.3e-06	16/29	62	(Mercer <i>et al.</i> , 1995)
048L	40360 38921	479	55.6	poly(A) polymerase catalytic subunit				(Gershon <i>et al.</i> , 1991)
E1L		479		VAC	0.0	478/479	99	(Goebel <i>et al.</i> , 1990).
E1L		479		VAR-I	0.0	472/479	98	(Shchelkunov <i>et al.</i> , 1995)
MC031L		470		MCV subtype I	1.5e-177	114/173	65	(Senkevich <i>et al.</i> , 1997)
049L	42570	737	85.9	85.9k protein				(Ahn <i>et al.</i> , 1990a)
E2L	40357	737		VAC	0.0	735/737	99	(Goebel <i>et al.</i> , 1990).
E2L		737		VAR-I	0.0	731/737	99	(Shchelkunov <i>et al.</i> , 1995)
MC032L		748		MCV subtype I	8.3e-127	59/198	29	(Senkevich <i>et al.</i> , 1997)
050L	43269 42697	190	21.5	dsRNA dependent PK inhibitor, host range				(Chang <i>et al.</i> , 1992) (Chang <i>et al.</i> , 1995b)
E3L		190		VAC	1.4e-129	188/190	98	(Goebel <i>et al.</i> , 1990).
E3L		192		VAR-BSH	8.6e-126	111/114	97	(Shchelkunov <i>et al.</i> , 1995)
		1175		dsRNA specific ADA (rat)	7.2e-12	22/47	46	(O'Connell <i>et al.</i> , 1995)
		1226		dsRNA specific ADA (human)	2.8e-09	21/47	44	(Kim <i>et al.</i> , 1994)
		551		human protein kinase p68	3.8e-05	22/42	52	(Meurs <i>et al.</i> , 1990)
				INF inducible kinase family	>0.00099			
051L	44103 43324	259	29.8	RNA polymerase subunit rpo30, VITF-1				(Ahn <i>et al.</i> , 1990a)
E4L		259		VAC	1.6e-182	258/259	99	(Broyles and Pennington, 1990)
E4L		259		VAR-BSH	3.2e-180	255/259	98	(Goebel <i>et al.</i> , 1990)
MC034L		444		MCV subtype I	1.2e-84	107/171	62	(Shchelkunov <i>et al.</i> , 1995)
		39		orf virus	6.7e-10	21/39	53	(Senkevich <i>et al.</i> , 1996)
		243		African swine fever virus	0.00034	17/36	47	(Mercer <i>et al.</i> , 1995)
				TFIIS family	<0.0096			(Vydelingum <i>et al.</i> , 1993)
052R	44180	331	39.1	39.1k protein				(Goebel <i>et al.</i> , 1990)
ESR	45175	331		VAC	1.2e-235	329/331	99	(Goebel <i>et al.</i> , 1990)
ESR		341		VAR	3.1e-223	312/331	94	(Shchelkunov <i>et al.</i> , 1995)
		332		Taterapox	7.1e-225	300/314	95	(Douglas and Dumbell, 1996)
		329		Camelpox	1.4e-221	206/220	93	(Douglas and Dumbell, 1996)
		319		Cowpox	1.5e-202	271/303	89	(Douglas and Dumbell, 1996)
		256		Ectromelia	3.8e-153	218/245	88	(Douglas and Dumbell, 1996)
MC038R		276		MCV subtype I	8.3e-109	94/152	61	(Senkevich <i>et al.</i> , 1997)
053R	45312	567	66.7	66.7k protein				(Goebel <i>et al.</i> , 1990)

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF ^a	START STOP	AA ^b	kDa ^c	name / (putative) function / homologies ^d	BLAST ^e expect	BLAST ^e AA id	HSS ^f (%)	references
left	terminal	region:						
E6R	567			VAR	0.0	555/567	97	(Shchelkunov <i>et al.</i> , 1995)
MC037R	565			MCV subtype 1	7.2e-247	258/451	57	(Senkevich <i>et al.</i> , 1997)
054R	47082	166	19.5	17k myristylprotein				(Martin <i>et al.</i> , 1997)
E7R	47582	166		VAC	9.7e-116	166/166	100	(Goebel <i>et al.</i> , 1990)
E7R	60			VAR-1 (BSH: E6.5R)	2.7e-36	53/60	88	(Shchelkunov <i>et al.</i> , 1995)
055R	47695	273	31.9	31.9k protein				(Earl <i>et al.</i> , 1986)
ENR	48516	273		VAC	4.5e-195	272/273	99	(Goebel <i>et al.</i> , 1990)
E8R	273			VAR	9.9e-192	266/273	99	(Shchelkunov <i>et al.</i> , 1993a)
MC038R	276			MCV subtype 1	8.3e-109	94/152	97	(Senkevich <i>et al.</i> , 1997)
056L	51543	1006	116.9	DNA polymerase				(Earl <i>et al.</i> , 1986)
E9L	48523	1006		VAC	0.0	1005/10	99	(Goebel <i>et al.</i> , 1990)
E9L	1005			VAR BSH	0.0	06	98	(Shchelkunov <i>et al.</i> , 1995)
	1008			Orf virus	0.0	598/608	51	(Mercer <i>et al.</i> , 1996)
	988			FPV	0.0	199/388	60	(Binns <i>et al.</i> , 1987)
MC039L	1004			MCV subtype 1	0.0	179/294	58	(Senkevich <i>et al.</i> , 1997)
	964			C. biennis poxvirus	2.6e-77	175/297	34	(Mustafa and Yuen, 1991)
				DNA polymerase family	>6.0e-06	28/82		
057R	51575	95	10.9	10.9k protein				(Goebel <i>et al.</i> , 1990)
E10R	51862	95		VAC	1.2e-65	93/95	97	(Goebel <i>et al.</i> , 1990)
E10R	95			VAR	3.1e-64	90/95	100	(Shchelkunov <i>et al.</i> , 1993a)
MC040R	101			MCV subtype 1	5.2e-44	58/95	94	(Senkevich <i>et al.</i> , 1997)
058L	52246	129	14.9	14.9k protein				(Goebel <i>et al.</i> , 1990)
E11L	51857	129		VAC	3.3e-89	129/129	100	(Goebel <i>et al.</i> , 1990)
E11L	129			VAR	4.2e-87	125/129	96	(Shchelkunov <i>et al.</i> , 1995)
MC041L	132			MCV subtype 1	1.8e-30	31/96	32	(Senkevich <i>et al.</i> , 1997)
059L	52691	152	17.6	77.6k protein (f1)				(Goebel <i>et al.</i> , 1990)
OIL	52233	666		VAC	6.9e-101	151/152	99	(Goebel <i>et al.</i> , 1990)
QIL	666			VAR-BSH	3.4e-92	137/152	90	(Shchelkunov <i>et al.</i> , 1995)
MC042L	783			MCV subtype 1	1.5e-22	39/105	37	(Senkevich <i>et al.</i> , 1997)
				leu zipper, bipartite nuclear targeting sequence				(Goebel <i>et al.</i> , 1990)
060L	54189	405	47.4	77.6k protein (f2)				(Goebel <i>et al.</i> , 1990)
OIL	52972	666		VAC	5.8e-277	399/400	99	(Goebel <i>et al.</i> , 1990)
QIL	666			VAR-1	1.7e-269	383/400	95	(Shchelkunov <i>et al.</i> , 1995)
MC042L	783			MCV subtype 1	2.7e-51	38/104	36	(Senkevich <i>et al.</i> , 1997)
061L	54555	108	12.4	glutaredoxin 1				(Ahn and Moss, 1992a)
	54229							(Johnson <i>et al.</i> , 1991)
O2L	108			VAC	2.0e-74	108/108	100	(Goebel <i>et al.</i> , 1990)
Q2L	108			VAR	4.9e-72	104/108	96	(Shchelkunov <i>et al.</i> , 1995)
	106			human glutaredoxin	3.2e-31	49/106	46	(Fernando <i>et al.</i> , 1994)
				glutaredoxin family	>9.0e-05			
062L	55639	312	35.9	35.9k protein				(Schmitt and Stunnenberg, 1988)
IIL	54701	312		VAC	4.7e-208	310/312	99	(Goebel <i>et al.</i> , 1990)
KIL	312			VAR-BSH	4.8e-205	305/312	97	(Shchelkunov <i>et al.</i> , 1995)
MC044L	310			MCV subtype 1	3.8e-110	163/307	53	(Senkevich <i>et al.</i> , 1996)
	1451			(transcription initiation protein (S. cerevisiae))	0.029	10/28	35	(Hansen <i>et al.</i> , 1996)
063L	55867	73	8.5	8.5k protein				(Schmitt and Stunnenberg, 1988)
I2L	55646	73		VAC	5.5e-50	73/73	100	(Goebel <i>et al.</i> , 1990)
K2L	73			VAR	5.5e-50	73/73	100	(Shchelkunov <i>et al.</i> , 1995)
MC045L	72			MCV subtype 1	3.5e-18	20/33	60	(Senkevich <i>et al.</i> , 1996)
	887			hypothetical yeast protein	8.1e-05	9/24	37	S48422
064L	56677	269	30.0	DNA binding phospho-protein (F4L interacting)				(Schmitt and Stunnenberg, 1988)
	55868							(Davis and Mathews, 1993)
I3L	269			VAC	2.1e-173	267/269	99	(Goebel <i>et al.</i> , 1990)
K3L	269			VAR	2.5e-172	265/269	98	(Shchelkunov <i>et al.</i> , 1995)
MC046L	288			MCV subtype 1	9.6e-66	61/149	40	(Senkevich <i>et al.</i> , 1996)
	209			FPV I3 protein	8.4e-35	23/66	34	A48563
065L	59075	771	87.8	ribonucleotide reductase (large subunit)				(Schmitt and Stunnenberg, 1988)
	56760							(Tengelsen <i>et al.</i> , 1988)
I4L	771			VAC	0.0	771/771	100	(Goebel <i>et al.</i> , 1990)
K4L	771			VAR	0.0	761/771	98	(Shchelkunov <i>et al.</i> , 1995)
				ribonucleotide red. family	>1.8e-05			
066L	59342	79	8.8	8.8k protein				(Schmitt and Stunnenberg, 1988)
I5L	59103	79		VAC	6.3e-49	79/79	100	(Goebel <i>et al.</i> , 1990)
K5L	79			VAR	1.2e-47	76/79	96	(Shchelkunov <i>et al.</i> , 1995)
MC047L	82			MCV subtype 1	2.6e-17	27/73	36	(Senkevich <i>et al.</i> , 1996)
	81			FPV 9.1k protein	1.4e-12	13/38	34	(Binns <i>et al.</i> , 1988)
	321			formate dep. nitrit reductase	0.00022	7/18	38	(Fleischmann <i>et al.</i> , 1995)
	496			protein (H. influenzae)				
				permease (b. subtilis)	0.00031	12/43	27	gi:2415386
067L	60509	382	43.5	43.5k protein				(Schmitt and Stunnenberg, 1988)
I6L	59361	382		VAC	8.6e-268	382/382	100	(Goebel <i>et al.</i> , 1990)
K6L	382			VAR	3.1e-267	380/382	99	(Shchelkunov <i>et al.</i> , 1995)
MC048L	406			MCV subtype 1	2.1e-99	44/119	36	(Senkevich <i>et al.</i> , 1996)

ORF ^a	START STOP	AA ^b	kDa ^c	name / (putative) function / homologies ^d	BLAST ^e expect	BLAST ^e AA id	HSS ^f (%)	references
	left	terminal	region:					
			390	FPV I6 protein mitochondrial energy transfer proteins signature	1.4e-86	50/136	36	E48563, P12925 (Goebel <i>et al.</i> , 1990)
068L	61773	423	49.0	core protein, topoisomerase II				(Schmitt and Stunnenberg, 1988)
	60502							(Kane and Shuman, 1993)
I7L		423		VAC	0.0	420/423	99	(Goebel <i>et al.</i> , 1990)
K7L		423		VAR	1.5e-306	419/423	99	(Shchelkunov <i>et al.</i> , 1995)
MC049L		515		MCV subtype I	1.9e-199	126/207	60	(Senkevich <i>et al.</i> , 1996)
		421		FPV I7 protein	8.1e-180	185/340	54	F48563
		464		Amsacta moorei poxvirus	3.2e-14	14/47	29	(Hall and Moyer, 1991)
069R	61776	676	77.6	NPH-II, NTPase, RNA helicase				(Shuman, 1992), (Koonin and Senkevich, 1992)
	63809							(Goebel <i>et al.</i> , 1990)
I8R		676		VAC	0.0	674/676	99	(Goebel <i>et al.</i> , 1990)
K8R		676		VAR	0.0	665/676	98	(Shchelkunov <i>et al.</i> , 1995)
MC050R		684		MCV subtype I	7.6e-227	144/272	52	(Senkevich <i>et al.</i> , 1997)
		682		FPV virus I8FPV	4.2e-206	98/178	55	(Binns <i>et al.</i> , 1988)
				61 matches mainly to RNA helicase family	<0.38			
070L	65588	591	68.0	68k protein				(Schmitt and Stunnenberg, 1988)
G1L	63813	591		VAC	0.0	590/591	99	(Goebel <i>et al.</i> , 1990)
H1L		591		VAR-I	0.0	582/591	98	(Shchelkunov <i>et al.</i> , 1995)
MC056L		593		MCV subtype I	1.2e-217	183/361	50	(Senkevich <i>et al.</i> , 1997)
		341		FPV	9.4e-75	45/101	44	H48563
071L	65920	111	12.8	12.8k protein				(Schmitt and Stunnenberg, 1988)
	65585							(Meis and Condit, 1991)
G3L		111		VAC	7.6e-74	111/111	100	(Goebel <i>et al.</i> , 1990)
H3L		111		VAR	2.4e-71	108/111	97	(Shchelkunov <i>et al.</i> , 1995)
MC057L		108		MCV subtype I	0.00012	15/45	33	(Senkevich <i>et al.</i> , 1997)
072R	65914	220	25.8	IDT-dependent protein				(Meis and Condit, 1991)
G2R	66576	220		VAC	1.9e-155	220/220	100	(Goebel <i>et al.</i> , 1990)
H2R		220		VAR	1.1e-151	214/220	97	(Shchelkunov <i>et al.</i> , 1995)
MC058R		246		MCV subtype I	2.7e-36	42/135	31	(Senkevich <i>et al.</i> , 1997)
073L	66920	124	14.0	glutaredoxin 2 membrane protein				(Gvakharia <i>et al.</i> , 1996)
	66546							(Jensen <i>et al.</i> , 1996)
H4L		124		VAR	4.0e-83	123/124	99	(Shchelkunov <i>et al.</i> , 1995)
G4L		124		VAC	7.5e-83	123/124	99	(Goebel <i>et al.</i> , 1990)
MC059L		126		MCV subtype I	1.1e-21	21/51	41	(Senkevich <i>et al.</i> , 1997)
074R	66923	434	49.9	49.8k protein				(Goebel <i>et al.</i> , 1990)
G5R	68227	434		VAC	1.6e-305	432/434	99	(Goebel <i>et al.</i> , 1990)
H5R		434		VAR	1.9e-299	423/434	97	(Shchelkunov <i>et al.</i> , 1995)
MC60R		437		MCV subtype I	1.0e-55	56/119	47	(Senkevich <i>et al.</i> , 1997)
		1300		HS CGI protein	0.015	22/82	26	(Print <i>et al.</i> , 1994)
075R	68235	63	7.3	RNA polymerase subunit rpo7				(Amegadzie <i>et al.</i> , 1992), (Meis and Condit, 1991)
	68426							(Goebel <i>et al.</i> , 1990)
G5.5R		63		VAC	1.1e-40	63/63	100	(Goebel <i>et al.</i> , 1990)
H5.5R		63		VAR	1.1e-39	61/63	96	(Shchelkunov <i>et al.</i> , 1995)
MC061R		63		MCV subtype I	9.3e-27	41/63	65	(Senkevich <i>et al.</i> , 1997)
				35 matches mainly to RNA polymerases	<0.54			
076R	68428	165	19.0	18.9k protein				(Goebel <i>et al.</i> , 1990)
G6R	68925	165		VAC	3.8e-116	162/165	98	(Goebel <i>et al.</i> , 1990)
H6R		165		VAR	1.5e-116	164/165	99	(Shchelkunov <i>et al.</i> , 1995)
MC062R		195		MCV subtype I	3.0e-32	27/57	47	(Senkevich <i>et al.</i> , 1997)
077L	70005	371	42.0	42.0k protein				(Schmitt and Stunnenberg, 1988)
G7L	68890	371		VAC	5.2e-255	370/371	99	(Goebel <i>et al.</i> , 1990)
H7L		371		VAR	7.1e-255	369/371	99	(Shchelkunov <i>et al.</i> , 1995)
MC065L		402		MCV subtype I	2.0e-109	69/145	47	(Senkevich <i>et al.</i> , 1997)
078R	70036	260	29.9	VLTF-1, late transcription factor				(Keck <i>et al.</i> , 1990)
	70818							(Wright <i>et al.</i> , 1991)
G8R		260		VAC	8.6-184	259/260	99	(Goebel <i>et al.</i> , 1990)
H8R		260		VAR-I	3.1e-183	258/260	99	(Shchelkunov <i>et al.</i> , 1995)
MC067R		260		MCV subtype I	8.5e-136	185/260	71	(Senkevich <i>et al.</i> , 1997)
		260		FPV virus FPO	3.3e-129	175/250	67	(Binns <i>et al.</i> , 1988)
079R	70838	340	38.9	37k myristylprotein				(Martin <i>et al.</i> , 1997)
G9R	71860	340		VAC	3.7e-237	317/319	99	(Goebel <i>et al.</i> , 1990)
H9R		340		VAR	9.1e-236	315/319	98	(Shchelkunov <i>et al.</i> , 1995)
MC068R		342		MCV subtype I	4.8e-79	59/127	46	(Senkevich <i>et al.</i> , 1997)
		336		FPV virus FPI	3.9e-65	59/124	47	(Binns <i>et al.</i> , 1988)
080R	71861	250	27.3	25k myristylprotein IMV virion protein				(Franke <i>et al.</i> , 1990)
	72613							(Martin <i>et al.</i> , 1997)
L1R		250		VAC	1.8e-175	250/250	100	(Goebel <i>et al.</i> , 1990)
M1R		250		VAR	6.4e-170	249/250	99	(Shchelkunov <i>et al.</i> , 1995)
MC069R		243		MCV subtype I	6.5e-103	145/243	59	(Senkevich <i>et al.</i> , 1997)
		243		FPV virus FP2	6.2e-95	128/243	52	(Binns <i>et al.</i> , 1988)
		212		VAC F9L	1.6e-07	20/58	34	(Goebel <i>et al.</i> , 1990)
		212		VAR C13L	3.1e-07	20/58	34	(Shchelkunov <i>et al.</i> , 1995)

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF ^a	START STOP	AA ^b	kDa ^c	name / (putative) function / homologies ^d	BLAST ^e expect	BLAST ^e AA id	HSS ^f (%)	references
	left	terminal	region:					
			213	MCV subtype I MC016L	1.6e-0.7	13/57	22	(Senkevich <i>et al.</i> , 1997)
			215	swinepox	3.3e-0.5	15/51	29	(Massung <i>et al.</i> , 1993)
081R	72645	87	10.3	10.3k protein				(Plucienniczak <i>et al.</i> , 1985)
L2R	72908	87		VAC	3.9e-57	87/87	100	(Goebel <i>et al.</i> , 1990)
M2R		87		VAR	4.0e-56	85/87	97	(Shchelkunov <i>et al.</i> , 1995)
MC070R		93		MCV subtype I	0.064	18/80	22	(Senkevich <i>et al.</i> , 1997)
		504		Na ⁺ dependent phosphate transporter <i>C. elegans</i>	6.9e-05	10/39	25	(Wilson <i>et al.</i> , 1994)
		233		ATPase subunit T. cruzi	0.013	16/44	36	U38184
		2336		Ca ²⁺ channel rat	5.2e+0.2	6/25	24	(Dubel <i>et al.</i> , 1992)
		2238		Ca ²⁺ channel mouse	7.1e+0.2	6/25	24	(Coppola <i>et al.</i> , 1994)
		1559		ABC transporter yeast	0.40	12/40	30	X97560
082L	73950	350	40.6	40.6k protein				(Plucienniczak <i>et al.</i> , 1985)
L3L	72898	350		VAC	2.2e-251	346/350	98	(Goebel <i>et al.</i> , 1990)
M3L		349		VAR	1.5e-241	296/306	96	(Shchelkunov <i>et al.</i> , 1995)
MC072L		310		MCV subtype I	1.5e-88	64/136	47	(Senkevich <i>et al.</i> , 1997)
		301		FPV F4 protein	1.1e-80	58/134	43	(Binns <i>et al.</i> , 1988)
083R	73975	251	28.5	core protein VP8				(Yang and Bauer, 1988)
	74730			DNA/RNA binding protein				(Baylis and Smith, 1997)
L4R		251		VAC	5.6e-170	251/251	100	(Goebel <i>et al.</i> , 1990)
M4R		251		VAR	3.7-169	250/251	99	(Shchelkunov <i>et al.</i> , 1995)
MC073R		254		MCV subtype I	1.7e-76	36/59	61	(Senkevich <i>et al.</i> , 1997)
		253		FPV virus FP5	6.4e-55	29/57	50	(Binns <i>et al.</i> , 1988)
084R	74740	128	15.1	15.1k protein				(Goebel <i>et al.</i> , 1990)
L5R	75126	128		VAC 14.0k protein	2.9e-89	127/128	99	(Shchelkunov <i>et al.</i> , 1995)
M5R		128		VAR	2.0-87	125/128	97	(Drillien <i>et al.</i> , 1987)
		129		FPV FP6	8.1e-16	19/45	42	(Senkevich <i>et al.</i> , 1997)
MC074R		146		MCV subtype I	0.073	10/18	55	(Reppert <i>et al.</i> , 1995)
		152		melatonin receptor <i>D. rerio</i>	0.44	15/66	222	
085R	75083	153	17.9	dimeric virion protein				(Holzer & Falkner, unpubl.)
J1R	75544	153		VAC	6.0e-103	152/153	99	(Goebel <i>et al.</i> , 1990)
L1R		159		VAR-I	1.4e-101	149/153	97	(Shchelkunov <i>et al.</i> , 1995)
		147		capripox CF7	6.5e-54	53/90	58	(Gershon and Black, 1989b)
		148		myxoma MF7	4.8e-51	54/93	58	(Jackson and Bults, 1992)
MC075R		183		MCV subtype I	1.9e-47	47/93	50	(Senkevich <i>et al.</i> , 1997)
		148		FPV FP7	1.3e-35	37/84	44	(Drillien <i>et al.</i> , 1987)
086R	75560	177	20.0	thymidine kinase				(Hruby and Ball, 1982)
	76093							(Weir and Moss, 1983)
J2R		177		VAC	5.7e-125	175/177	98	(Goebel <i>et al.</i> , 1990)
L2R		177		VAR	2.7e-122	170/177	96	(Shchelkunov <i>et al.</i> , 1995)
				38 matches mainly to thymidine kinase family	<0.18			
087R	76159	333	38.9	poly(A) polymerase su,				(Gershon <i>et al.</i> , 1991)
	77160			2'methyl transferase				(Gershon and Moss, 1993)
J3R		333		VAC	8.7e-136	330/333	99	(Goebel <i>et al.</i> , 1990)
L3R		333		VAR-BSH	9.8e-233	326/333	97	(Shchelkunov <i>et al.</i> , 1995)
		338		myxoma	5.7e-288	247/333	74	(Jackson and Bults, 1990)
MC076R		343		MCV subtype I	1.4e-135	79/144	54	(Senkevich <i>et al.</i> , 1997)
		308		FPV VP39	1.7e-96	125/267	46	(Binns <i>et al.</i> , 1988)
088R	77075	185	21.3	RNA pol subunit rpo22				(Broyles and Moss, 1986)
J4R	77632	185		VAC	1.2e-125	185/185	100	(Goebel <i>et al.</i> , 1990)
L4R		185		VAR-BSH	7.9e-125	182/185	98	(Shchelkunov <i>et al.</i> , 1995)
		185		myxoma	1.5e-86	124/185	67	(Jackson and Bults, 1990)
MC077R		187		MCV subtype I	1.9e-76	73/132	55	(Senkevich <i>et al.</i> , 1997)
		186		FPV	2.1e-73	72/135	53	(Binns <i>et al.</i> , 1988)
089L	78101	133	15.2	15.2k protein				(Plucienniczak <i>et al.</i> , 1985)
J5L	77700	133		VAC	2.4e-95	133/133	100	(Goebel <i>et al.</i> , 1990)
L5L		133		VAR-I	2.4e-94	131/133	98	(Shchelkunov <i>et al.</i> , 1995)
MC078L		134		MCV subtype I	5.7e-45	60/127	47	(Senkevich <i>et al.</i> , 1997)
		137		FPV	1.4e-43	60/130	46	(Drillien <i>et al.</i> , 1987)
		377		VAR-I A16L (BSH:A17L)	0.049	7/28	25	(Shchelkunov <i>et al.</i> , 1995)
		378		VAC A16L	0.049	7/28	25	(Goebel <i>et al.</i> , 1990)
090R	78207	1286	146.9	RNA pol subunit rpo147				(Broyles and Moss, 1986)
J6R	82067	1286		VAC	0.0	1283/1286	99	(Goebel <i>et al.</i> , 1990)
L6R		1286		VAR	0.0	1275/1286	99	(Shchelkunov <i>et al.</i> , 1995)
MC079R		1289		MCV subtype I	0.0	556/760	73	(Senkevich <i>et al.</i> , 1997)
				100 matches to RNA pol (large subunit) family	<3.7e-07			
091L	82579	171	19.7	protein tyrosine/serine phosphatase				(Rosel <i>et al.</i> , 1986)
	82064							(Guan <i>et al.</i> , 1991)
H1L		171		VAC	2.0e-117	170/171	99	(Goebel <i>et al.</i> , 1990)
I1L		171		VAR	1.1e-114	166/171	97	(Shchelkunov <i>et al.</i> , 1995)
		171		raccoonpox	6.0e-111	157/171	91	B47452
		172		myxoma virus	1.5e-77	83/138	60	(Mossman <i>et al.</i> , 1995a)
		173		rabbit fibroma virus	1.8e-77	46/80	57	(Mossman <i>et al.</i> , 1995a)
MC082L		169		MCV subtype I	1.4e-65	60/114	52	(Senkevich <i>et al.</i> , 1997)
				protein phosphatase family	>2.8e-05			

ORF ^a	START STOP	AA ^b	kDa ^c	name / (putative) function / homologies ^d	BLAST ^e expect	BLAST ^e AA id	HSS ^f (%)	references
left	terminal	region:						
092R	82593	189	21.5	21.5k protein				(Rosel <i>et al.</i> , 1986)
H2R	83162	189		VAC	5.2e-134	188/189	99	(Goebel <i>et al.</i> , 1990)
I2R		189		VAR	1.4e-133	188/189	99	(Shchelkunov <i>et al.</i> , 1995)
MC083R		191		MCV subtype I	1.4e-71	95/181	52	(Senkevich <i>et al.</i> , 1997)
		142		myxoma	1.3e-65	93/142	65	(Jackson and Bults, 1990)
093L	84139	324	37.5	immunodominant env protein p35; IMV				(Rosel <i>et al.</i> , 1986)
	83165			membrane-associated				(Chertov <i>et al.</i> , 1991)
H3L		324		VAC	3.3e-231	322/324	99	(Takahashi <i>et al.</i> , 1994)
I3L		325		VAR-BSH	1.7e-225	311/320	97	(Goebel <i>et al.</i> , 1990)
MC084L		298		MCV subtype I	1.1e-36	38/117	32	(Shchelkunov <i>et al.</i> , 1995)
								(Senkevich <i>et al.</i> , 1996)
094L	86527	795	93.6	RAP 94 (RNA-pol assoc. transcr. spec. factor)				(Ahn and Moss, 1992b)
	84140			VAC				(Kane and Shuman, 1992)
H4L		795		VAR	0.0	791/795	99	(Goebel <i>et al.</i> , 1990)
I4L		795		VAR	0.0	780/795	98	(Shchelkunov <i>et al.</i> , 1995)
MC085L		791		MCV subtype I	0.0	327/546	59	(Senkevich <i>et al.</i> , 1996)
		804		Orf virus	0.0	96/131	73	(Fleming <i>et al.</i> , 1993)
		484		FPV L1L protein	2.4e-181	91/176	51	2209386A
095R	86713	203	22.3	late transcription factor				(Kovacs and Moss, 1996)
	87324			VLTF-4				(Rosel <i>et al.</i> , 1986)
H5R		203		VAC	1.8e-128	202/203	99	(Goebel <i>et al.</i> , 1990)
I5R		221		VAR	5.1e-102	91/97	93	(Shchelkunov <i>et al.</i> , 1995)
		227		orf virus F3R	3.1e-14	29/69	42	(Fleming <i>et al.</i> , 1993)
		220		MCV subtype I	3.1e-09	28/64	43	(Senkevich <i>et al.</i> , 1997)
		705		nucleolin Xenopus	0.00041	18/57	31	(Messmer and Dreyer, 1993)
				31 matches to glu/asp rich proteins	E<0.52			
096R	87325	314	36.7	DNA topoisomerase I				(Shuman and Moss, 1987)
	88269							(Rosel <i>et al.</i> , 1986)
H6R		314		VAC	0.0	314/314	100	(Goebel <i>et al.</i> , 1990)
I6R		314		VAR-BSH	9.5e-220	312/314	99	(Shchelkunov <i>et al.</i> , 1995)
		314		shope fibroma virus	8.5e-141	119/170	70	(Upton <i>et al.</i> , 1990b)
		318		orf virus	5.2e-128	82/138	59	(Fleming <i>et al.</i> , 1993)
MC087R		323		MCV subtype I	1.6e-121	111/202	54	(Senkevich <i>et al.</i> , 1997)
		316		FPV L3R	2.9e-113	159/303	52	(Zantinge <i>et al.</i> , 1996)
				21 matches to topoisomerase family				
097R	88306	146	17.0	17.0k protein				(Rosel <i>et al.</i> , 1986)
H7R	88746	146		VAC	2.1e-98	144/146	98	(Goebel <i>et al.</i> , 1990)
I7R		146		VAR	6.7e-96	141/146	96	(Shchelkunov <i>et al.</i> , 1995)
MC088R		143		MCV subtype I	4.3e-30	45/115	39	(Senkevich <i>et al.</i> , 1997)
098R	88790	844	96.8	mRNA capping enzyme, large subunit				(Morgan <i>et al.</i> , 1984)
	91324			VAC				(Niles <i>et al.</i> , 1986)
D1R		844		VAR-BSH	0.0	842/844	99	(Goebel <i>et al.</i> , 1990)
F1R		844		VAR-BSH	0.0	830/844	98	(Shchelkunov <i>et al.</i> , 1995)
MC090R		950		MCV subtype I	0.0	322/64	64	(Senkevich <i>et al.</i> , 1997)
		836		shope fibroma virus	0.0	243/305	79	(Upton <i>et al.</i> , 1991b)
		868		ASV NP868R	0.0033	17/55	30	(Pena <i>et al.</i> , 1993)
099L	91723	146	16.9	structural protein				(Niles <i>et al.</i> , 1986)
	91283							(Dyster and Niles, 1991)
D2L		146		VAC	5.9e-98	146/146	100	(Goebel <i>et al.</i> , 1990)
F2L		146		VAR (BSH: F3L)	1.5e-97	145/146	99	(Shchelkunov <i>et al.</i> , 1995)
MC091L		143		Rabbit fibroma virus	2.0e-27	13/33	39	(Upton <i>et al.</i> , 1991b)
		170		MCV subtype I	1.1e-20	19/41	46	(Senkevich <i>et al.</i> , 1996)
100R	91716	233	27.6	27k structural protein				(Dyster and Niles, 1991)
D3R	92417	237		VAC	3.8e-167	136/142	95	(Goebel <i>et al.</i> , 1990)
F2R		237		VAR I:F3R	1.5e-162	131/142	92	(Shchelkunov <i>et al.</i> , 1995)
		241		shope fibroma virus	9.3e-20	27/100	27	(Upton <i>et al.</i> , 1991b)
MC092R		268		MCV subtype I	3.5e-18	16/39	41	(Senkevich <i>et al.</i> , 1997)
		206		rabbit fibroma virus C3	1.6e-09	26/96	27	(Strayer <i>et al.</i> , 1991)
101R	92417	218	25.1	uracil DNA glycosylase				(Upton <i>et al.</i> , 1993)
D4R	93073	218		VAC	1.4e-157	217/218	99	(Goebel <i>et al.</i> , 1990)
F4R		218		VAR-BSH	5.1e-157	216/218	99	(Shchelkunov <i>et al.</i> , 1995)
		218		shope fibroma virus	1.5e-117	151/218	69	(Upton <i>et al.</i> , 1993)
MC093R		226		MCV subtype I	8.4e-91	65/113	57	(Senkevich <i>et al.</i> , 1997)
		218		FPV FPD4	3.1e-88	116/216	53	(Tartaglia <i>et al.</i> , 1990)
		297		uracil DNA glycosylase UL2	0.019	8/14	57	L34064
				gallid herpesvirus 1				
102R	93105	785	90.4	90.4k ATP/GTP binding protein				(Niles <i>et al.</i> , 1986)
	95462							(Shchelkunov <i>et al.</i> , 1993c)
D5R		785		VAC	0.0	780/785	99	(Goebel <i>et al.</i> , 1990)
F5R		785		VAR	0.0	774/785	98	(Shchelkunov <i>et al.</i> , 1995)
		786		shope fibroma C5	0.0	283/450	62	(Strayer <i>et al.</i> , 1991)
		791		MCV subtype I	0.0	184/334	55	(Senkevich <i>et al.</i> , 1997)
		791		FPV virus FPD5	0.0	170/345	49	(Tartaglia <i>et al.</i> , 1990)
MC094R		942		C29E6.4 C. elegans	0.72	16/56	28	(Wilson <i>et al.</i> , 1994)
103R	95503	637	73.9	early transcription factor				(Broyles and Fesler, 1990)
	97416			VETF-1				(Gershon and Moss, 1990)

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ORF*	START STOP	AA*	kDa*	name / function	(putative) / homologues*	BLAST ^a expect	BLAST ^a AA id	HSS ^b (%)	references
	left	terminal	region:						
D6R		637		VAC		0.0	635/637	99	(Goebel <i>et al.</i> , 1990)
F6R		637		VAR-I		0.0	633/637	99	(Shchelkunov <i>et al.</i> , 1995)
		635		shope fibroma virus		0.0	212/262	80	(Strayer <i>et al.</i> , 1991)
MC095R		635		MCV subtype I		0.0	199/263	75	(Senkevich <i>et al.</i> , 1997)
		605		FPV		0.0	188/263	71	(Binns <i>et al.</i> , 1990)
		648		Choristoneura biennis EPV		2.7e-08	24/72	33	(Tartaglia <i>et al.</i> , 1990)
		648		Amsacta moorei EPV		4.2e-06	24/77	31	(Yuen <i>et al.</i> , 1991)
		706		African swine fever virus		1.5e-05	13/38	34	(Hall and Moyer, 1991)
									(Yancz <i>et al.</i> , 1993)
104R	97443	161	17.9	RNA polymerase					(Ahn <i>et al.</i> , 1990b)
	97928			subunit rpol8					(Quick and Broyles, 1990)
D7R		161		VAC		1.4e-108	160/161	99	(Goebel <i>et al.</i> , 1990)
F7R		161		VAR		2.2e-106	156/161	96	(Shchelkunov <i>et al.</i> , 1995)
		163		rabbit fibroma C8		3.4e-76	108/161	67	(Strayer <i>et al.</i> , 1991)
MC097R		161		MCV subtype I		4.0e-70	99/158	62	(Senkevich <i>et al.</i> , 1997)
		161		FPV D7		5.4e-66	95/160	59	(Binns <i>et al.</i> , 1990)
105L	98805	304	35.4	virion transmembrane					(Niles and Seto, 1988)
	97891			protein, carbonic					(Niles <i>et al.</i> , 1986)
				anhydrase-like					(Maa <i>et al.</i> , 1990)
D8L		304		VAC		2.3e-212	297/304	97	(Goebel <i>et al.</i> , 1990)
F8L		304		VAR		2.5e-209	291/304	95	(Shchelkunov <i>et al.</i> , 1995)
		304		Camelpox virus		1.1e-207	290/304	95	X97857
		303		Ectromelia virus		2.2e-207	195/207	94	X97856
		304		Monkeypox virus		3.0e-207	287/304	94	X97855
		304		Cowpox virus		9.8e-206	285/304	93	X97858
				Carbonic anhydrase family		>4.9e-13			
106R	98847	213	25.0	25k mutT-like protein					(Koonin, 1993)
	99488								(Niles <i>et al.</i> , 1986)
D9R		213		VAC		1.6e-146	212/213	99	(Goebel <i>et al.</i> , 1990)
F9R		213		VAR		5.3e-145	209/213	98	(Shchelkunov <i>et al.</i> , 1995)
		218		rabbit fibroma		1.7e-75	105/203	51	(Strayer <i>et al.</i> , 1991)
MC098R		212		MCV subtype I		5.3e-67	54/111	48	(Senkevich <i>et al.</i> , 1997)
		78		FPV D9		2.0e-13	25/51	49	(Tartaglia <i>et al.</i> , 1990)
MC099R		229		MCV subtype I		0.0041	13/31	41	(Senkevich <i>et al.</i> , 1997)
		248		VAR-I F10R		0.018	14/32	43	(Shchelkunov <i>et al.</i> , 1995)
		225		FPV D10		0.14	15/34	44	(Tartaglia <i>et al.</i> , 1990)
		248		VAC D10R		0.23	11/26	42	(Goebel <i>et al.</i> , 1990)
107R	99485	248	28.9	29k mutT-like protein					(Koonin, 1993)
	100231								(Niles <i>et al.</i> , 1986)
D10R		248		VAC		7.4e-173	245/248	98	(Goebel <i>et al.</i> , 1990)
F10R		248		VAR-I		5.4e-173	245/248	98	(Shchelkunov <i>et al.</i> , 1995)
		260		shope fibroma D10		3.8e-72	96/202	47	(Strayer <i>et al.</i> , 1991)
MC099R		229		MCV subtype I		1.4e-54	44/100	44	(Senkevich <i>et al.</i> , 1997)
		225		FPV D10		1.1e-45	45/102	44	(Binns <i>et al.</i> , 1990)
		218		shope fibroma D9		1.9e-06	19/54	35	(Strayer <i>et al.</i> , 1991)
		212		MCV subtype I MC098R		0.13	12/21	57	(Senkevich <i>et al.</i> , 1997)
		136		mutator Synechocystis		0.23	12/27	44	D90899
		213		VAC D9R		0.24	11/26	42	(Goebel <i>et al.</i> , 1990)
		213		VAR F9R		0.24	11/26	42	(Shchelkunov <i>et al.</i> , 1995)
		169		mutator M. jannaschii		0.39	13/25	52	(Bult <i>et al.</i> , 1996)
108L	102127	631	72.4	nucleoside triphosphate					(Broyles and Moss, 1987)
	100232			phosphohydrolase I,					(Rodriguez <i>et al.</i> , 1986)
				DNA helicase					(Koonin and Senkevich, 1992)
D11L		631		VAC		0.0	629/631	99	(Goebel <i>et al.</i> , 1990)
N1L		631		VAR		0.0	626/631	99	(Shchelkunov <i>et al.</i> , 1995)
MC100R		634		MCV subtype I		7.3e-286	392/627	62	(Senkevich <i>et al.</i> , 1996)
		637		FPV protein 5		2.8e-275	214/357	59	S42251
		370		Rabbit fibroma C14 protein		1.8e-176	244/368	66	F36819
		648		AmEPV		6.0e-142	81/159	50	(Hall and Moyer, 1991)
		648		Choristoneura biennis EPV		1.1e-136	81/158	51	(Yuen <i>et al.</i> , 1991)
		89		Swinepox virus		1.2e-34	60/89	67	(Massung <i>et al.</i> , 1993)
		1098		ASF		1.6e-13	26/89	29	(Baylis <i>et al.</i> , 1993)
		1085		RAD26 (yeast)		5.1e-05	16/45	35	(Huang <i>et al.</i> , 1994)
		769		HS transcription activator		0.00093	10/22	45	(Okabe <i>et al.</i> , 1992)
				NTPase family		>5.1e-5			
109L	103025	287	33.3	mRNA capping enzyme,					(Niles <i>et al.</i> , 1989)
	102162			transcription initiation					(Weinrich and Hruby, 1986)
				factor VITF					(Vos <i>et al.</i> , 1991)
D12L		287		VAC		2.0e-198	285/287	99	(Goebel <i>et al.</i> , 1990)
N2L		287		VAR		9.8e-198	284/287	99	(Shchelkunov <i>et al.</i> , 1995)
		287		Swinepox virus		4.1e-160	220/287	76	(Massung <i>et al.</i> , 1993)
MC101L		295		MCV subtype I		5.8e-126	171/279	61	(Senkevich <i>et al.</i> , 1996)
		289		FPV protein 6		3.4e-113	114/215	53	S42252
110L	104711	551	61.9	rifampicin resistance					(Tartaglia and Paoletti, 1985)
	103056			gene, IMV protein					(Weinrich and Hruby, 1986)
D13L		551		VAC		0.0	551/551	100	(Goebel <i>et al.</i> , 1990)
N3L		551		VAR		0.0	547/551	99	(Shchelkunov <i>et al.</i> , 1995)
		551		Swinepox virus		4.5e-286	357/506	70	(Massung <i>et al.</i> , 1993)
MC102L		547		MCV subtype I		5.4e-248	298/494	60	(Senkevich <i>et al.</i> , 1996)
		552		FPV protein 7		6.6e-223	182/305	59	S42253
		584		Heliothis armigera EPV		9.5e-51	54/107	50	(Osborne <i>et al.</i> , 1996)

ORF ^a	START STOP	AA ^b	kDa ^c	name / function	(putative) / homologues ^d	BLAST ^e expect	BLAST ^f AA id	HSS ^g (%)	references
left terminal region:									
111L	105187 104735	150	16.9	late gene trans-activator, VLT-2					(Weinrich and Hruby, 1986)
A1L		150		VAC		6.8e-103	149/150	99	(Keck <i>et al.</i> , 1993)
A1L		150		VAR		6.8e-103	149/150	99	(Goebel <i>et al.</i> , 1990)
MC103L		169		MCV subtype I		6.3e-54	74/147	50	(Shchelkunov <i>et al.</i> , 1995)
		154		FPV protein 8		2.8e-50	50/87	57	(Senkevich <i>et al.</i> , 1996)
									S42254
112L	105882	224	26.3	late gene trans-activator					(Weinrich and Hruby, 1986)
A2L	105208			VAC					(Passarelli <i>et al.</i> , 1996)
A2L		224		VAR		1.3e-158	224/224	100	(Goebel <i>et al.</i> , 1990)
MC104L		224		MCV subtype I		1.3e-158	224/224	100	(Shchelkunov <i>et al.</i> , 1995)
		228		orf virus		6.4e-127	172/222	77	(Senkevich <i>et al.</i> , 1996)
		606				6.8e-30	43/66	65	(Mercer <i>et al.</i> , 1995)
113L	106109	76	8.9	8.9k protein					
	105879	76		VAC-WR		1.6e-47	73/76	96	(Weinrich and Hruby, 1986)
A3L		76		VAR-BSH (I:A2.5L)		2.1e-47	71/76	93	(Shchelkunov <i>et al.</i> , 1995)
MC105L		70		MCV subtype I		9.8e-12	26/63	41	(Senkevich <i>et al.</i> , 1996)
114L	108058	644	72.6	major core protein P4b					(Rosel and Moss, 1985)
A2L	106124	644		VAC		0.0	643/644	99	(Goebel <i>et al.</i> , 1990)
A4L		644		VAR-BSH (I:A3L)		0.0	636/644	98	(Shchelkunov <i>et al.</i> , 1995)
MC106L		675		MCV subtype I		8.9e-272	227/357	63	(Senkevich <i>et al.</i> , 1996)
		657		FPV Major core protein P4b		9.1e-220	169/299	56	(Binns <i>et al.</i> , 1989)
115L	108929 108111	272	29.9	membrane associated core protein					(Demkowicz <i>et al.</i> , 1992)
A4L		281		VAC		1.1e-145	180/187	96	(Cudmore <i>et al.</i> , 1996)
A5L		271		VAR-BSH (I: A4L)		1.1e-112	165/178	92	(Goebel <i>et al.</i> , 1990)
		268		Thermoproteus phage I		1.9e-09	38/127	29	(Shchelkunov <i>et al.</i> , 1995)
		5179		human mucin		4.5e-07	34/139	24	(Neumann and Zillig, 1990)
				many matches to Pro-rich proteins					(Gum <i>et al.</i> , 1994)
116R	108967	164	19.0	RNA pol subunit rpo19					(Ahn <i>et al.</i> , 1992)
A5R	109461	164		VAC		5.8e-110	164/164	100	(Goebel <i>et al.</i> , 1990)
A5R		164		VAR-I (BSH:A6R)		7.0e-109	162/164	98	(Shchelkunov <i>et al.</i> , 1995)
MC108R		165		MCV subtype I		3.3e-51	82/151	53	(Senkevich <i>et al.</i> , 1997)
		167		FPV		3.3e-51	72/161	44	(Kumar and Boyle, 1990)
				54 matches/glu-rich proteins		<0.51			
117L	110576	372	43.1	43.1k protein					
A6L	109458	372		VAC		1.2e-248	371/372	99	(Goebel <i>et al.</i> , 1990)
A7L		372		VAR-BSH (I: A6L)		1.1e-244	364/372	97	(Shchelkunov <i>et al.</i> , 1995)
MC109L		461		MCV subtype I		4.0e-99	132/367	35	(Senkevich <i>et al.</i> , 1996)
		339		FPV ORF 2 protein		1.9e-95	111/279	39	(B60013)
118L	112732	710	82.3	VETF 82k subunit					(Gershon and Moss, 1990)
A7L	110600	710		VAC		0.0	708/710	99	(Goebel <i>et al.</i> , 1990)
A8L		710		VAR-BSH (I: A7L)		0.0	700/710	98	(Shchelkunov <i>et al.</i> , 1995)
MC110L		707		MCV subtype I		0.0	240/374	64	(Senkevich <i>et al.</i> , 1996)
119R	112786	288	33.6	33.6k protein					(Van Meir and Wittek, 1988)
A8R	113652	288		VAC		5.3e-198	287/288	99	(Goebel <i>et al.</i> , 1990)
A8R		288		VAR-I (BSH:A9R)		3.1e-195	284/288	98	(Shchelkunov <i>et al.</i> , 1995)
MC111R		435		MCV subtype I		4.4e-94	100/169	59	(Senkevich <i>et al.</i> , 1997)
120L	113929	94	10.5	10.5k protein					(Van Meir and Wittek, 1988)
A10L	113645	95		VAR-BSH (I: A9L)		9.0e-59	78/79	98	(Shchelkunov <i>et al.</i> , 1995)
A9L		99		VAC		9.4e-55	82/91	90	(Goebel <i>et al.</i> , 1990)
MC112L		128		MCV subtype I		1.0e-29	47/71	66	(Senkevich <i>et al.</i> , 1996)
		69		orf virus		3.0e-16	27/45	60	(Mercer <i>et al.</i> , 1995)
121L	116605 113930	891	102.2	major core protein P4a					(Van Meir and Wittek, 1988)
A10L		891		VAC		0.0	883/891	99	(Vanslyke <i>et al.</i> , 1991)
A11L		892		VAR-BSH (I: A10L)		0.0	442/463	95	(Goebel <i>et al.</i> , 1990)
MC113L		889		MCV subtype I		5.8e-289	99/177	55	(Shchelkunov <i>et al.</i> , 1995)
									(Senkevich <i>et al.</i> , 1996)
122R	116620	318	36.1	36.1k protein					(Goebel <i>et al.</i> , 1990)
A11R	117576	318		VAC		3.5e-212	318/318	100	(Goebel <i>et al.</i> , 1990)
A11R		319		VAR-I (BSH: A12R)		2.7e-154	242/277	87	(Shchelkunov <i>et al.</i> , 1995)
MC114R		304		MCV subtype I		2.9e-98	92/154	59	(Senkevich <i>et al.</i> , 1997)
		148		FPV 4a gene		1.9e-13	18/32	56	(A20158)
123L	118141	187	20.0	virion protein					(Takahashi <i>et al.</i> , 1994)
A12L	117578	192		VAC		4.8e-127	127/128	99	(Goebel <i>et al.</i> , 1990)
A13L		189		VAR-BSH (I: A12L)		5.9e-64	101/144	70	(Shchelkunov <i>et al.</i> , 1995)
MC115L		178		MCV subtype I		5.9e-37	39/83	46	(Senkevich <i>et al.</i> , 1996)
124L	118377 118165	70	7.6	structural protein IMV membrane protein					(Takahashi <i>et al.</i> , 1994)
		70		p8		2.4e-42	66/69	95	(Jensen <i>et al.</i> , 1996)
A13L		68		VAC		4.1e-20	37/64	57	(Goebel <i>et al.</i> , 1990)
A14L				VAR-BSH (I: A13L)					(Shchelkunov <i>et al.</i> , 1995)
125L	118757 118485	90	10.0	structural protein IMV membrane protein					(Takahashi <i>et al.</i> , 1994)
				p16					(Jensen <i>et al.</i> , 1996)

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ORF ^a	START STOP	AA ^b region:	kDa ^c	name / (putative) function / homologies ^d	BLAST ^e expect	BLAST ^e AA id	HSS ^f (%)	references
left	terminal	region:						
A14L	90			VAC	5.3e-62	90/90	100	(Goebel <i>et al.</i> , 1990)
A15L	90			VAR-BSH (I: A14L)	5.3e-61	88/90	97	(Shchelkunov <i>et al.</i> , 1995)
MC118L	94			MCV subtype I	7.3e-22	31/72	43	(Senkevich <i>et al.</i> , 1996)
	125			human interferon inducible protein	0.23	15/49	30	(Deblandre <i>et al.</i> , 1995)
126L	119209	94	11.0	11k protein				
A15L	118925	94		VAC	4.1e-63	94/94	100	(Goebel <i>et al.</i> , 1990)
A16L	94			VAR-BSH (I: A15L)	1.0e-61	92/94	97	(Shchelkunov <i>et al.</i> , 1995)
MC120L	96			MCV subtype I	6.7e-08	17/51	33	(Senkevich <i>et al.</i> , 1996)
127L	120326	377	43.4	35k myristylprotein				(Martin <i>et al.</i> , 1997)
A16L	119193	378		VAC	6.3e-288	327/327	100	(Goebel <i>et al.</i> , 1990)
A17L	377			VAR-BSH (I: A16L)	1.5e-283	368/377	97	(Shchelkunov <i>et al.</i> , 1995)
MC121L	364			MCV subtype I	6.5e-110	45/115	39	(Senkevich <i>et al.</i> , 1996)
128L	120940	203	23.0	IMV membrane protein morphogenesis factor				(Krijnse-Locker <i>et al.</i> , 1996)
	120329							(Rodriguez <i>et al.</i> , 1995)
A17L	203			VAC	1.0e-141	201/203	99	(Wolfe <i>et al.</i> , 1996)
A18L	203			VAR-BSH (I: A17L)	1.0e-141	201/203	99	(Goebel <i>et al.</i> , 1990)
MC122L	179			MCV subtype I	1.4e-47	36/81	44	(Shchelkunov <i>et al.</i> , 1995)
								(Senkevich <i>et al.</i> , 1996)
129R	120955	493	56.8	DNA helicase				(Koonin and Senkevich, 1992)
	122436			DNA dependent ATPase				(Bayliss and Condit, 1995)
A18R	493			VAC	0.0	488/493	98	(Goebel <i>et al.</i> , 1990)
A19R	493			VAR-I (BSH: A19R)	0.0	478/493	96	(Shchelkunov <i>et al.</i> , 1995)
MC123R	694			MCV subtype I	5.3e-167	203/403	50	(Senkevich <i>et al.</i> , 1997)
	450			Bacteriophage T5 D10 helicase-like protein	0.0066	13/36	36	P11107
130L	122650	77	8.3	8.3kb protein				(Goebel <i>et al.</i> , 1990)
A19L	122417	77		VAC	2.9e-50	77/77	100	(Goebel <i>et al.</i> , 1990)
A19L	76			VAR-I (BSH: A20L)	1.2e-34	54/64	84	(Shchelkunov <i>et al.</i> , 1995)
MC124L	78			MCV subtype I	1.5e-13	14/37	37	(Senkevich <i>et al.</i> , 1996)
	1721			HS RIZ, zink finger protein	0.0060	7/16	43	(Buyse <i>et al.</i> , 1995)
131L	123004	117	13.6	13.6k protein				(Goebel <i>et al.</i> , 1990)
A21L	122651	117		VAC	5.3e-83	117/117	100	(Goebel <i>et al.</i> , 1990)
A22L	117			VAR-BSH (I: A20L)	7.2e-82	115/117	98	(Shchelkunov <i>et al.</i> , 1995)
MC125L	114			MCV subtype I	2.8e-28	23/41	56	(Senkevich <i>et al.</i> , 1996)
132R	123003	426	49.1	49.1k protein				(Goebel <i>et al.</i> , 1990)
A20R	124283	426		VAC	7.6e-298	423/426	99	(Goebel <i>et al.</i> , 1990)
A21R	426			VAR	1.6e-294	418/426	98	(Shchelkunov <i>et al.</i> , 1995)
MC126R	476			MCV subtype I	3.2e-95	34/131	25	(Senkevich <i>et al.</i> , 1997)
	1118			Pichia klyveri DNA pol	0.069	12/54	22	Y11606
133R	124213	187	21.9	21.9k protein				(Goebel <i>et al.</i> , 1990)
A22R	124776	187		VAR-I (BSH: A23R)	1.1e-126	182/187	97	(Shchelkunov <i>et al.</i> , 1995)
A22R	176			VAC	1.2e-122	174/176	98	(Goebel <i>et al.</i> , 1990)
MC127R	282			MCV subtype I	5.8e-43	35/85	41	(Senkevich <i>et al.</i> , 1997)
134R	124796	382	44.6	44.6k protein				(Goebel <i>et al.</i> , 1990)
A23R	125944	382		VAC	4.2e-269	382/382	100	(Goebel <i>et al.</i> , 1990)
A23R	382			VAR-I (BSH: A24R)	1.7e-265	377/382	98	(Shchelkunov <i>et al.</i> , 1995)
MC128R	383			MCV subtype I	3.5e-136	83/143	58	(Senkevich <i>et al.</i> , 1997)
135R	125966	1155	132.4	RNA pol subunit rpo132				(Hooda-Dhingra <i>et al.</i> , 1990)
	129436							(Amegadzie <i>et al.</i> , 1991b)
A24R	1164			VAC	0.0	794/796	99	(Goebel <i>et al.</i> , 1990)
	1164			CPX rpo132	0.0	794/795	99	(Patel and Pickup, 1989)
A25R	1164			VAR-BSH (I: A24R)	0.0	789/795	99	(Shchelkunov <i>et al.</i> , 1995)
MC129R	1165			MCV subtype I	0.0	441/565	78	(Senkevich <i>et al.</i> , 1997)
	1162			orf virus	0.0	166/258	64	U33419
				101 matches to RNA pol beta subunit family	<0.036			
right	terminal	region:						
136L	129638	65	7.5	150k CPX-ATI (f)				(Funahashi <i>et al.</i> , 1988)
A25L	129441	65		VAC	1.3e-41	64/65	98	(Goebel <i>et al.</i> , 1990)
	1284			Cowpox (CPX-ATI)	3.2e-15	28/30	93	(Funahashi <i>et al.</i> , 1988)
137L	130916	230	27.1	27.1k protein (f)				(Amegadzie <i>et al.</i> , 1991a)
A30L	130224	498		VAR-BSH (I: A29L)	3.1e-158	216/227	95	(Shchelkunov <i>et al.</i> , 1995)
A26L	322			VAC (ATI flanking protein)	5.6e-142	195/197	98	(Goebel <i>et al.</i> , 1990)
MC131L	513			MCV subtype I	2.1e-12	19/59	32	(Senkevich <i>et al.</i> , 1996)
MC133L	546			MCV subtype I	4.2e-11	12/40	30	(Senkevich <i>et al.</i> , 1996)
MC130L	451			MCV subtype I	2.3e-10	14/40	35	(Senkevich <i>et al.</i> , 1996)
	702			VAR-I A23L (BSH: A29L)	0.0021	12/37	32	(Shchelkunov <i>et al.</i> , 1995)
	726			Camelpox	0.051	11/37	29	(Meyer and Rziha, 1993)
138L	131298	110	12.5	14k membrane protein				(Rodriguez and Esteban, 1987)
	130966			EEV protein				(Rodriguez and Smith, 1990)
A27L	110			fusion protein				(Gong <i>et al.</i> , 1990)
A31L	110			VAC	3.3e-70	108/110	98	(Goebel <i>et al.</i> , 1990)
	110			VAR-BSH (I: A30L)	1.1e-69	107/110	97	(Shchelkunov <i>et al.</i> , 1995)
	117			Camelpox virus	1.5e-69	106/110	96	(Meyer <i>et al.</i> , 1994)
	110			Cowpox virus	1.6e-69	107/110	97	(Meyer <i>et al.</i> , 1994)

ORF ^a	START STOP	AA ^b	kDa ^c	name / (putative) function / homologies ^d	BLAST ^e expect	BLAST ^f AA id	HSS ^g (%)	references
	left	terminal	region:					
			110	Ectromelia virus	6.7e-68	105/110	95	(Meyer <i>et al.</i> , 1994)
			110	Monkeypox virus	8.3e-67	103/110	93	(Meyer <i>et al.</i> , 1994)
			89	Orf virus	4.8e-15	22/57	38	(Naase <i>et al.</i> , 1991)
MC133L			188	Myxoma virus	2.5e-12	18/33	54	(Jackson <i>et al.</i> , 1996)
			546	MCV subtype 1	1.5e-11	26/58	44	(Senkevich <i>et al.</i> , 1996)
			148	Capripox virus HM2 protein	2.6e-10	21/42	50	(Gershon <i>et al.</i> , 1989)
MC131L			513	MCV subtype 1	1.5e-05	18/58	31	(Senkevich <i>et al.</i> , 1996)
139L	131739	146	16.3	16.3k protein				(Amegadzie <i>et al.</i> , 1991a)
A28L	131299	146		VAC	1.7e-103	146/146	100	(Goebel <i>et al.</i> , 1990)
A31.5L		146		VAR-BSH (I: A31L)	2.9e-100	141/146	96	(Shchelkunov <i>et al.</i> , 1995)
		140		Myxoma virus	1.3e-55	30/52	57	(Jackson <i>et al.</i> , 1996)
		140		Capripox virus HM3 protein	3.3e-55	30/49	61	(Gershon <i>et al.</i> , 1989)
MC134L		141		MCV subtype 1	1.0e-53	31/52	59	(Senkevich <i>et al.</i> , 1996)
		143		Amsacta moorei poxvirus	2.0e-14	16/36	44	(Hall and Moyer, 1991)
140L	132657	305	35.4	RNA pol subunit rpo35				(Amegadzie <i>et al.</i> , 1991a)
A29L	131740	305		VAC	3.6e-215	304/305	99	(Goebel <i>et al.</i> , 1990)
A32L		305		VAR-BSH	7.5e-211	297/305	97	(Shchelkunov <i>et al.</i> , 1995)
MC135L		303		MCV subtype 1	7.0e-98	51/103	49	(Senkevich <i>et al.</i> , 1996)
		126		Capripox virus	2.2e-54	46/61	75	(Gershon <i>et al.</i> , 1989)
141L	132853	77	8.7	8.7k protein				(Amegadzie <i>et al.</i> , 1991a)
A30L	132620	77		VAC	5.5e-48	77/77	100	(Goebel <i>et al.</i> , 1990)
A33L		77		VAR	5.5e-48	77/77	100	(Shchelkunov <i>et al.</i> , 1995)
MC136L		67		MCV subtype 1	9.2e-16	18/40	45	(Senkevich <i>et al.</i> , 1996)
142R	133013	125	14.4	14.4k protein				(Smith <i>et al.</i> , 1991)
A31R	133390	124		VAC	2.0e-84	118/124	95	(Goebel <i>et al.</i> , 1990)
A34R		140		VAR	1.6e-79	111/114	97	(Shchelkunov <i>et al.</i> , 1995)
MC138R		117		MCV subtype 1	6.2e-24	39/98	39	(Senkevich <i>et al.</i> , 1997)
143L	134169	269	30.8	30.8k protein				(Smith <i>et al.</i> , 1991)
	133360			ATP/GTP binding motif A				(Koonin <i>et al.</i> , 1993)
A32L		300		VAC	6.4e-190	268/269	99	(Goebel <i>et al.</i> , 1990)
A35L		270		VAR	1.6e-186	263/269	97	(Shchelkunov <i>et al.</i> , 1995)
MC140L		249		MCV subtype 1	7.6e-95	58/94	61	(Senkevich <i>et al.</i> , 1996)
144R	134287	185	20.6	EEV glycoprotein				(Roper <i>et al.</i> , 1996)
A33R	134844	185		VAC	2.1e-124	182/185	98	(Goebel <i>et al.</i> , 1990)
A36R		184		VAR	1.8e-121	103/112	91	(Shchelkunov <i>et al.</i> , 1995)
		185		Ectromelia	2.8e-113	165/185	89	(Roper <i>et al.</i> , 1996)
145R	134868	168	19.6	EEV glycoprotein				(Duncan and Smith, 1992a)
	135374			virulence factor				(McIntosh and Smith, 1996)
				actin microvilli inducer				(Wolfe <i>et al.</i> , 1997)
A34R		168		VAC	1.2e-117	165/168	98	(Goebel <i>et al.</i> , 1990)
A37R		168		VAR-I	1.7e-117	164/168	97	(Shchelkunov <i>et al.</i> , 1995)
		167		FPV ORFs BamHI 2.8,11 hepatic	<0.056	16/66	24	(Tomley <i>et al.</i> , 1988)
				lectins homologs				
		199		HS early T-cell activation	0.0038	12/38	31	(Hamann <i>et al.</i> , 1993)
				antigen CD69				
MC143R		159		MCV subtype 1	0.080	12/48	25	(Senkevich <i>et al.</i> , 1997)
				17 matches to lectins				
146R	135418	176	20.0	20.0k protein				(Smith <i>et al.</i> , 1991)
A35R	135948	176		VAC	1.4e-126	176/176	100	(Goebel <i>et al.</i> , 1990)
A38R		60		VAR-I	2.9e-37	57/60	95	(Shchelkunov <i>et al.</i> , 1995)
MC145R		233		MCV subtype 1	1.2e-07	18/55	32	(Senkevich <i>et al.</i> , 1997)
147R	136015	208	23.8k	EEV membrane protein				(Parkinson and Smith, 1994)
	136641			virulence factor				(Smith <i>et al.</i> , 1991)
A36R		221		VAC	2.8e-143	140/141	99	(Goebel <i>et al.</i> , 1990)
A39R		216		VAR	2.1e-89	138/177	77	(Shchelkunov <i>et al.</i> , 1995)
				19 matches to asn/ser-rich proteins	<0.41			
148R	136705	263	29.3	29.3k protein				
A37R	137496	263		VAC	6.8e-183	261/262	99	(Goebel <i>et al.</i> , 1990)
A40R		68		VAR	4.9e-37	61/67	91	(Shchelkunov <i>et al.</i> , 1995)
149L	138589	277	31.5	31.5k protein				(Amegadzie <i>et al.</i> , 1991a)
A38L	137756	277		VAC	9.3e-198	274/277	98	(Goebel <i>et al.</i> , 1990)
A41L		277		VAR	1.6e-187	259/277	93	(Shchelkunov <i>et al.</i> , 1995)
		303		Rattus norvegicus CD47	3.9e-24	23/86	26	(Nishiyama <i>et al.</i> , 1997)
		324		MM integrin assoc. protein	1.0e-21	23/86	26	(Lindberg <i>et al.</i> , 1993)
		323		human CD47 precursor	5.0e-19	28/86	32	(Campbell <i>et al.</i> , 1992)
150R	138606	83	9.4	semaphorin-like protein (f1)				(Kolodkin <i>et al.</i> , 1993)
	138857							
A39R		403		VAC	8.0e-46	73/76	96	(Goebel <i>et al.</i> , 1990)
A42R		74		VAR-I	8.6e-44	67/71	94	(Shchelkunov <i>et al.</i> , 1995)
151R	139163	210	23.9	semaphorin-like protein (f2)				(Kolodkin <i>et al.</i> , 1993)
	139795							
A39R		403		VAC	3.0e-147	209/210	99	(Goebel <i>et al.</i> , 1990)
A43R		139		VAR (I:A44R)	1.8e-68	91/105	86	(Shchelkunov <i>et al.</i> , 1995)
		653		semaphorin-like protein	1.7e-20	29/79	36	(Ensser and Fleckenstein, 1995)
				Alcelaphine herpesvirus				
				37 matches to semaphorin				

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GENOMIC SEQUENCE OF THE MVA STRAIN

ORF*	START STOP	AA*	kDa*	name / (putative) function / homologies*	BLAST* expect	BLAST* AA id	HSS* (%)	references
left	terminal	region:						
/collapsin gene family								
152R	139821 140327	168	19.4	NK cell receptor homolog lectin-like protein				(Scheiflinger et al., unpubl.) (Smith et al., 1991)
A40R		168		VAC	6.6e-97	134/137	97	(Goebel et al., 1990)
A45R		61		VAR-I (BSH: A43.5R)	9.6e-36	54/59	91	(Shchelkunov et al., 1995)
		233		HS natural killer (NK) cell protein group 2-A, B	4.5e-11	20/74	27	(Houchins et al., 1991)
		240		HS type II membrane protein	6.9e-11	16/36	44	(Adamkiewicz et al., 1994)
		182		MM NK cell receptor	5.5e-09	16/36	44	(Giorda et al., 1992)
		179		HS CD 94	1.7e-07	11/29	37	(Chang et al., 1995a)
				127 matches to lectins including NK cell surface proteins and snake venoms				
153L	141025	219	25.1	25.1k protein				(Smith et al., 1991)
A41L	140366	219		VAC	1.9e-158	218/219	99	(Goebel et al., 1990)
A44L		218		VAR-BSH (I: A46L)	1.4e-152	152/159	95	(Shchelkunov et al., 1995)
		244		VAC B29R/C23L	0.0076	12/53	22	(Goebel et al., 1990)
		258		Rabbit fibroma virus T1	0.057	13/49	26	(Upton et al., 1987)
154R	141197 141583	128	14.5	profilin-like protein				(Blasco et al., 1991)
A42R		133		VAC	1.2e-87	85/87	97	(Smith et al., 1991)
A47R		133		VAR-I (BSH: A45R)	1.4e-85	82/87	94	(Goebel et al., 1990)
		140		HS profilin	2.2e-23	19/45	42	(Shchelkunov et al., 1995)
				10 matches profilin family				(Kwiatkowski and Bruns, 1988)
155R	141621 142193	190	22.1	class I membrane glycoprotein				(Smith et al., 1991)
A43R		194		VAC	1.5e-137	162/164	98	(Duncan and Smith, 1992b)
A48R		195		VAR-I (BSH: A46R)	1.9e-128	101/109	92	(Goebel et al., 1990)
		51		HS leukocyte antigen	0.096	7/23	30	(Shchelkunov et al., 1995)
156R	142201 142437	78	8.8	8.8k protein				(Smith et al., 1991)
		78		VAC-WR Salf6R	3.9e-45	78/78	100	(Smith et al., 1991)
		258		rabbit myosin heavy chain	0.00048	13/39	33	A02985
				144 matches to various asp/glu/lys-rich proteins				
157L	143577 142537	346	39.4	3 β -hydroxysteroid dehydrogenase (3 β -HSD)				(Moore and Smith, 1992)
A44L		346		VAC	4.5e-249	342/346	98	(Blasco et al., 1991)
A47L		210		VAR-BSH (I: A49L)	1.1e-136	185/195	94	(Goebel et al., 1990)
MC152R		354		MCV subtype I	8.2e-104	123/272	45	(Shchelkunov et al., 1995)
		369		FPV	3.1e-83	33/85	38	(Senkevich et al., 1996)
				matches to dihydroflavonol reductases, cholesterol dehydrogenases, UDP- galactose-4-epimerases	>2.8e-05			(Skinner et al., 1994)
158R	143624 143989	121	13.3	superoxide dismutase-like protein				(Blasco et al., 1991)
A45R		125		VAC	2.1e-82	94/96	97	(Smith et al., 1991)
A51R		125		VAR-I BSH A48R	1.1e-82	93/96	96	(Goebel et al., 1990)
				117 matches with superoxide dismutase family	<0.027			(Shchelkunov et al., 1995)
159R	143979	241	27.6	27.6k protein				(Smith et al., 1991)
A46R	144701	214		VAC	9.6e-167	238/240	99	(Goebel et al., 1990)
A52R		240		VAR-I (BSH: A49R)	5.6e-164	233/240	97	(Shchelkunov et al., 1995)
160L	145465	238	27.6	27.6k protein				(Goebel et al., 1990)
J1L	144749	244		VAR	5.1e-146	114/127	89	(Shchelkunov et al., 1995)
A47L		244		VAC	8.2e-135	121/127	95	(Goebel et al., 1990)
				integrin lipid binding motif				(Smith et al., 1991)
161R	145564	204	23.2	thymidylate kinase				(Smith et al., 1991)
A48R	146178	204		VAC	5.2e-140	204/204	100	(Goebel et al., 1990)
J2R		205		VAR	1.1e-137	161/165	97	(Shchelkunov et al., 1995)
				16 matches to thymidylate kinase family	<0.49			
162R	146202	162	18.8	18.8k protein				(Smith et al., 1991)
A49R	146690	162		VAC	6.0e-106	159/162	98	(Goebel et al., 1990)
J3R		162		VAR	2.4e-103	154/162	95	(Shchelkunov et al., 1995)
163R	146722	552	63.5	DNA ligase				(Kerr and Smith, 1989)
A50R	148380	552		VAC	0.0	547/552	99	(Goebel et al., 1990)
J4R		552		VAR-I	0.0	537/552	97	(Shchelkunov et al., 1995)
		922		HS DNA ligase III	2.1e-235	102/165	61	(Wei et al.,)
		559		shepe fibroma ligase	9.9e-213	95/200	47	(Parks et al., 1994)
		564		FPV ligase	3.0e-195	101/170	59	(Skinner et al., 1994)
				31 matches mainly to DNA ligase family	<0.029			
164R	148426	310	34.9	34.9k protein				(Antoine et al., 1996)
A51R	149358	334		VAC	1.5e-217	267/274	97	(Goebel et al., 1990)
J5R		334		VAR	9.1e-208	251/274	91	(Shchelkunov et al., 1995)

ORF*	START STOP	AA*	kDa*	name / (putative) function / homologies*	BLAST* expect	BLAST* AA id	HSS* (%)	references
left terminal region:								
				fusion of <i>AS1R/AS5R</i> ORFs				(Antoine <i>et al.</i> , 1996)
165R	149416	315	34.8	hemagglutinin				(Shida, 1986)
AS6R	150363	315		VAC	1.8e-211	312/315	99	(Goebel <i>et al.</i> , 1990)
J9R		313		VAR-I (BSH:J7R)	4.3e-178	183/238	76	(Shchelkunov <i>et al.</i> , 1995)
		310		raccoonpox	1.5e-91	74/104	71	(Cavallaro and Esposito, 1992)
				124 matches to various proteins	<0.34			
166R	150659	97	11.4	guanylate kinase (f)				(Smith <i>et al.</i> , 1991)
AS7R	150952	151		VAC	3.2e-62	94/97	96	(Goebel <i>et al.</i> , 1990)
J10R		151		VAR (BSH:J8R)	2.2e-57	88/97	90	(Shchelkunov <i>et al.</i> , 1995)
		198		MM guanylate kinase	4.3e-24	39/91	42	(Brady <i>et al.</i> , 1996)
		197		HS guanylate kinase	2.8e-20	35/91	38	(Brady <i>et al.</i> , 1996)
				21 matches mainly to guanylate kinases	<0.20			
167R	151103	300	34.3	serine/threonine protein kinase				(Howard and Smith, 1989)
	152005							(Banham and Smith, 1992)
B1R		300		VAC	7.1e-215	298/300	99	(Lin <i>et al.</i> , 1992)
B1R		300		VAR-I	2.7e-210	289/300	96	(Goebel <i>et al.</i> , 1990)
		283		VAC B12R	4.9e-49	27/53	50	(Shchelkunov <i>et al.</i> , 1995)
				100 matches mainly to protein kinase family	<0.00031			(Goebel <i>et al.</i> , 1990)
168R	152144	96	11.5	24.6k protein (f1)				
B2R	152434	219		VAC	8.5e-38	54/60	90	(Goebel <i>et al.</i> , 1990)
		149		histone H2A pea	0.59	16/50	32	P40281
169R	152289	143	16.1	24.6k protein (f2)				(Goebel <i>et al.</i> , 1990)
B2R	152720	219		VAC	5.7e-86	124/128	96	(Goebel <i>et al.</i> , 1990)
170R	152917	179	20.9	20.9k protein (f)				
B3R	153456	124		VAC	8.2e-33	51/56	91	(Goebel <i>et al.</i> , 1990)
		167		VAC WR	5.3e-45	51/56	91	(Smith <i>et al.</i> , 1991)
		92		VAR-GAR H5R	3.4e-06	19/28	67	U18339
171R	153683	177	21.4	65k ank-like protein virulence factor (f1)				(Howard <i>et al.</i> , 1991)
	154216							(Mossman <i>et al.</i> , 1996)
B4R		558		VAC	8.5e-107	151/154	98	(Goebel <i>et al.</i> , 1990)
B6R		558		VAR-I (BSH:B5R)	1.7e-98	140/154	90	(Shchelkunov <i>et al.</i> , 1995)
172R	154107	409	47.7	65k ank-like protein virulence factor (f2)				(Howard <i>et al.</i> , 1991)
	155336							(Mossman <i>et al.</i> , 1996)
B4R		558		VAC	2.4e-283	195/201	97	(Goebel <i>et al.</i> , 1990)
B6R		558		VAR-I (BSH:B5R)	2.3e-270	185/201	92	(Shchelkunov <i>et al.</i> , 1995)
		483		MYX M-T5 protein	5.5e-10	19/57	33	(Mossman <i>et al.</i> , 1996)
		1765		MM ankyrin 3	9.7e-10	22/54	40	(Peters <i>et al.</i> , 1995)
		516		orf virus	1.8e-09	16/47	34	U34774
		574		VAC B18R	3.3e-09	11/23	47	(Goebel <i>et al.</i> , 1990)
		574		VAR-I B19R	3.6e-09	19/72	26	(Shchelkunov <i>et al.</i> , 1995)
		882		HS KIAA0379	5.1e-09	20/52	38	AB002377
		668		CPX host range gene	1.7e-08	14/47	29	(Spehner <i>et al.</i> , 1988)
		237		VAC WR hr gene	2.8e-08	15/47	31	(Kotwal and Moss, 1988a)
		472		VAC M1L	5.1e-07	23/81	28	(Goebel <i>et al.</i> , 1990)
		474		CPX O1L	8.7e-07	22/61	36	(Safronov <i>et al.</i> , 1996)
		446		VAR O1L	8.8e-07	23/81	28	(Shchelkunov <i>et al.</i> , 1995)
		437		CPX D1L	1.7e-06	8/27	29	(Safronov <i>et al.</i> , 1996)
		634		VAC C9L	7.8e-05			(Goebel <i>et al.</i> , 1990)
				159 matches including ankyrin proteins				
173R	155424	317	35.1	ps/hr protein/EEV gp42				(Takahashi-Nishimaki <i>et al.</i> , 1991)
	156377							(Engelstad <i>et al.</i> , 1992)
B5R		317		complement control protein	1.6e-232	312/317	98	(Isaacs <i>et al.</i> , 1992)
B7R		317		VAC	7.1e-220	294/316	93	(Goebel <i>et al.</i> , 1990)
		259		VAR-I (BSH:B6R)	2.1e-12	16/52	30	(Shchelkunov <i>et al.</i> , 1995)
				CPX D17L	<7.7e-05			(Safronov <i>et al.</i> , 1996)
				186 matches to complement control protein family				
174R	156474	173	20.2	20.2k protein				
B6R	156995	173		VAC	1.5e-121	173/173	100	(Goebel <i>et al.</i> , 1990)
B7R		65		VAR-BSH (I:B8R)	6.0e-40	62/65	95	(Shchelkunov <i>et al.</i> , 1995)
		685		NAD-protein ADP ribosyl-transferase phage T4	0.56	17/56	30	SXBPT4
175R	157033	177	20.7	20.7k protein				
B7R	157566	182		VAC	7.8e-129	95/108	87	(Goebel <i>et al.</i> , 1990)
		184		VAC C8L	0.16	9/44	20	(Goebel <i>et al.</i> , 1990)
		182		CPX D12L	0.49	8/36	22	(Safronov <i>et al.</i> , 1996)
				EF-hand calcium-binding domain				
176R	157621	226	26.0	31k interferon-gamma receptor (f)				(Upton <i>et al.</i> , 1992)
	158301							(Alcami and Smith, 1995)
B8R		272		VAC	3.3e-164	116/123	94	(Goebel <i>et al.</i> , 1990)
B8R		266		VAR-BSH (I:B9R)	3.0e-153	111/123	90	(Shchelkunov <i>et al.</i> , 1995)
		266		ECT	2.6e-151	110/123	89	(Mossman <i>et al.</i> , 1995b)
		274		swinepox C6	3.2e-09	12/31	38	(Massung <i>et al.</i> , 1993)

GENOMIC SEQUENCE OF THE MVA STRAIN

ORF ^a	START STOP	AA ^b	kDa ^c	name / (putative) function / homologies ^d	BLAST ^e expect	BLAST ^e AA id	HSS ^f (%)	references
left terminal region:								
177R	158458	72	8.3	8.3k protein				
B9R	158676	77		VAC				
		240		capripox T4 protein	3.0e-49	60/60	100	(Goebel <i>et al.</i> , 1990)
		237		shope fibroma virus	1.2e-09	16/44	36	M28823
					0.0057	15/50	30	F43692
178R	158639	158	17.9	17.9k protein				
B10R	159115	166		VAC	4.7e-110	146/146	100	(Goebel <i>et al.</i> , 1990)
		530		swinepox VC04	0.040	13/42	30	(Massung <i>et al.</i> , 1993)
		689		kelch protein D. melanogaster	0.14	12/54	27	(Xue and Cooley, 1993)
								(Senkevich <i>et al.</i> , 1993b)
179R	159187	74	8.5	8.5k protein				
B11R	159411	88		VAC	9.2e-43	70/73	95	(Goebel <i>et al.</i> , 1990)
				177 matches to glu/asn rich proteins				
180R	159478	283	33.3	protein kinase				(Howard and Smith, 1989)
B12R	160329	283		VAC	1.8e-207	282/283	99	(Goebel <i>et al.</i> , 1990)
		134		VAR-I	8.7e-26	31/54	57	(Shchelkunov <i>et al.</i> , 1995)
		300		VAC B1R	1.7e-54	26/53	49	(Goebel <i>et al.</i> , 1990)
		300		VAR-I B1R	7.7e-53	25/53	47	(Shchelkunov <i>et al.</i> , 1995)
				120 matches mainly to protein kinase family	<0.34			
181R	160437	116	13.0	ICE inhibitor / SPI-2 (f1)				(Kotwal and Moss, 1989)
B13R	160787			VAC				(Smith <i>et al.</i> , 1989)
		116		VAR-I (BSH:B12R)	3.0e-72	111/116	95	(Ray <i>et al.</i> , 1992)
		344		CPX crmA	2.7e-69	105/114	92	(Goebel <i>et al.</i> , 1990)
		341		VAC C12L (SPI-I)	2.8e-39	66/100	66	(Shchelkunov <i>et al.</i> , 1995)
		353		Ectromelia serpin	2.1e-23	25/34	73	(Pickup <i>et al.</i> , 1986)
		344		rabbitpox SPI-I	9.2e-23	24/34	70	(Goebel <i>et al.</i> , 1990)
		357		CPX SPI-I	5.5e-22	25/34	73	(Senkevich <i>et al.</i> , 1993b)
		355		VAR-I B25R (BSH:B21R)	1.4e-21	25/36	69	(Ali <i>et al.</i> , 1994)
		372		CPX serpin-like protein	1.7e-21	25/34	73	(Ali <i>et al.</i> , 1994)
		372		135 matches mainly to serpins	1.7e-36	25/36	69	(Shchelkunov <i>et al.</i> , 1995)
					<0.12			(Ali <i>et al.</i> , 1994)
182R	160762	222	24.9	ICE inhibitor/SPI-2 (f2)				see above
B14R	161430	222		VAC	6.2e-158	218/222	98	(Goebel <i>et al.</i> , 1990)
		345		VAC WR	9.4e-156	215/221	97	(Goebel <i>et al.</i> , 1990)
		345		rabbit pox SPI-2	1.6e-153	211/221	95	(Kotwal and Moss, 1989)
		341		CPX crmA	4.5e-148	203/220	92	(Ali <i>et al.</i> , 1994)
		344		VAR-I (BSH:B12R)	1.5e-146	203/220	92	(Pickup <i>et al.</i> , 1986)
B13R				309 matches see above	<1.3e-21			(Shchelkunov <i>et al.</i> , 1995)
183R	161506	143	16.7	16.7k protein				(Smith and Chan, 1991)
B15R	161937	149		VAC	3.6e-105	97/98	98	(Goebel <i>et al.</i> , 1990)
B14R		149		VAR-I (BSH:B13R)	9.1e-104	95/98	96	(Shchelkunov <i>et al.</i> , 1995)
		153		VAR-I D1L (BSH:D2L)	8.8e-31	25/52	48	(Shchelkunov <i>et al.</i> , 1995)
		181		VAC C16L/B22R	1.0e-26	25/52	48	(Goebel <i>et al.</i> , 1990)
		159		capripox T3A	1.4e-17	17/42	40	(Gershon and Black, 1989a)
		151		rabbit fibroma T3A	2.6e-07	17/44	38	(Upton <i>et al.</i> , 1987)
		190		VAC A52R	0.073	10/28	35	(Goebel <i>et al.</i> , 1990)
		149		VAC WR K7R	0.21	7/22	31	(Boursnell <i>et al.</i> , 1988)
		149		VAR-IC4R	0.30	7/22	31	(Shchelkunov <i>et al.</i> , 1995)
		161		CPX M6R	0.51	7/22	31	(Safronov <i>et al.</i> , 1996)
184R	162021	326	36.6	interleukin-1B receptor (IL-1BR)				(Alcami and Smith, 1992)
	163001			VAC-WR B15R	2.8e-229	323/326	99	(Spriggs <i>et al.</i> , 1992)
		326		CPX B16	2.3e-217	306/326	93	(Smith <i>et al.</i> , 1991)
B16R		290		VAC	4.4e-202	287/290	98	(Spriggs <i>et al.</i> , 1992)
B17R		69		VAR-I (BSH:deleted)	8.1e-38	59/68	86	(Goebel <i>et al.</i> , 1990)
		296		HS type II IL-1 receptor	1.7e-36	28/75	37	(Shchelkunov <i>et al.</i> , 1995)
				271 matches mainly to IL-1 receptors, growth factor receptors and Ig family proteins	<0.011			U64094
185L	164069	340	39.6	39.6k protein				
B17L	163047	340		VAC	4.8e-248	335/340	98	(Goebel <i>et al.</i> , 1990)
B15L		340		VAR-BSH (I:B18L)	2.7e-241	325/340	95	(Shchelkunov <i>et al.</i> , 1995)
186R	164209	574	68.0	68k ank-like protein				(Smith <i>et al.</i> , 1991)
B18R	165933	574		VAC	0.0	560/574	97	(Goebel <i>et al.</i> , 1990)
B19R		574		VAR-I (BSH:B16R)	0.0	539/574	93	(Shchelkunov <i>et al.</i> , 1995)
				100 matches mainly to poxvirus ankyrin proteins	<0.53			
187R	165999	234	27.5	surface antigen, IFN-alpha/beta receptor (f)				(Ueda <i>et al.</i> , 1990)
	166703			VAC (WR:B18R)				(Symons <i>et al.</i> , 1995)
B19R		353		VAR-I (BSH:B17R)	1.4e-163	218/233	93	(Colamonici <i>et al.</i> , 1995)
B20R		354		HS interleukin-1 receptor	1.53-149	111/133	83	(Goebel <i>et al.</i> , 1990)
		569		28 matches mainly to IL-1 receptors	0.0051	15/43	34	(Shchelkunov <i>et al.</i> , 1995)
					<0.53			(McMahan <i>et al.</i> , 1991)
188R	167202	70	8.2	8.2k protein (f)				

ORF ^a	START STOP	AA ^b	kDa ^c	name / (putative) function / homologies ^d	BLAST ^e expect	BLAST ^e AA id	HSS ^f (%)	references
left terminal region:								
B22R	167414	1897		VAR-BSH (I:B26R)	9.9e-23	31/38	81	(Shchelkunov <i>et al.</i> , 1995)
189R	167897	188	21.7	21.7k protein				
B22R	168463	181		VAC B22R/C16L	2.9e-111	95/104	91	(Goebel <i>et al.</i> , 1990)
D1L		153		VAR-I (BSH:D2L)	1.2e-88	66/71	92	(Shchelkunov <i>et al.</i> , 1995)
		149		VAC B15R	7.2e-19	25/52	48	(Goebel <i>et al.</i> , 1990)
		159		capripox T3A	8.0e-05	15/45	33	(Gershon and Black, 1989a)
		151		VACC6L	0.25	12/46	26	(Goebel <i>et al.</i> , 1990)
		156		VAR (I:D9L;BSH:D12L)	0.26	12/46	26	(Shchelkunov <i>et al.</i> , 1995)
190R/ 004L B23R D1L	168531 169232	233	26.9	45k ank-like protein (f2)				
		386		VAC (C17L/B23R)	6.2e-159	110/110	100	(Goebel <i>et al.</i> , 1990)
		91		VAR-BSH	9.1e-31	46/49	93	(Shchelkunov <i>et al.</i> , 1995)
		669		CPX host range	1.1e-13	22/50	44	(Spehner <i>et al.</i> , 1988)
		452		VAR-I D6L (BSH:D8L)	1.7e-11	21/50	42	(Shchelkunov <i>et al.</i> , 1995)
		574		VAR-I B19R (BSH: B16R)	1.2e-05	22/73	30	(Shchelkunov <i>et al.</i> , 1995)
		574		VAC B18R (WR: B17R)	8.6e-05	22/73	30	(Shchelkunov <i>et al.</i> , 1995)
		634		VACC9L	0.00011	11/24	45	(Goebel <i>et al.</i> , 1990)
		585		VAR-I GIR	0.00013	22/74	29	(Kotwal and Moss, 1988a)
		516		orf virus	0.0088	15/49	30	(Shchelkunov <i>et al.</i> , 1995)
		153		VAR-I D7L (BSH:D10L)	0.014	12/28	42	(Sullivan <i>et al.</i> , 1995b)
191R/ 003L B23R	169309 169617	102	12.1	45k ank-like protein (f1)				(Shchelkunov <i>et al.</i> , 1995)
		386		VAC C17L/B23R	1.3e-39	62/63	98	(Goebel <i>et al.</i> , 1990)
192R/ 002L G2R	170305 170835	176 355 348	19.7	secre. TNF receptor (f)				(Upton <i>et al.</i> , 1991a)
		326		CPX crmB	5.1e-71	76/83	91	(Hu <i>et al.</i> , 1994)
		326		VAR-BSH	1.0e-66	73/83	87	(Shchelkunov <i>et al.</i> , 1995)
		325		Myxoma virus T2	4.9e-30	21/37	56	(Upton <i>et al.</i> , 1991a)
		202		Rabbit fibroma Virus T2	1.8e-28	17/36	47	(Upton <i>et al.</i> , 1987)
		202		CPX C4L	8.7e-15	30/51	58	(Heller <i>et al.</i> , 1990)
B25R		346		HS TNF receptor	1.9e-08	14/26	53	(Safronov <i>et al.</i> , 1996)
		259		VAC (C19L/B25R)	0.00026	16/19	84	(Goebel <i>et al.</i> , 1990)
		277		human CD40L receptor	0.0015	11/24	45	(Stamenovic <i>et al.</i> , 1989)
				30 matches to TNF receptors and surface proteins	<0.39			
193R/ 001L B29R G5R	171267 171677	136 244 253 246 258 260	14.9	35k major secre. protein chemokine receptor (f)				(Patel <i>et al.</i> , 1990)
		244		VAC (C23L/B29R)	6.0e-57	41/42	97	(Graham <i>et al.</i> , 1997)
		253		VAR-I	8.9e-51	46/49	93	(Goebel <i>et al.</i> , 1990)
		246		CPX ORFB	5.6e-49	40/42	95	(Shchelkunov <i>et al.</i> , 1995)
		258		SFV T1 protein	2.5e-20	23/42	54	(Hu <i>et al.</i> , 1994)
		260		Myxoma virus T1/35kDa	1.5e-14	21/42	50	(Upton <i>et al.</i> , 1987)
								(Graham <i>et al.</i> , 1997)

^a Open reading frame coding for at least 65 amino acids (for exceptions see text); minor ORFs located in reverse orientation within large ORFs or ORFs located in the repeat regions of the ITRs (see text) are not listed; the MVA ORFs (boldface), listed consecutively as appearing in the genome, and homologs in the Copenhagen strain (in italics), in the variola strains and in the molluscum contagiosum, are listed in this row. Split ORFs are boxed.

^b Number of deduced amino acids (AA) encoded within an ORF.

^c Predicted M_r (kDa) for the unmodified protein.

^d The lowest Poisson probability determined by the BLAST search (Altschul *et al.*, 1990). The Expect value of 0.0 indicates a probability of zero that an alignment occurs by chance; low Expect values correspond to high homology and vice versa.

^e Amino acid identity (AA id) of first high-scoring segment pair in the BLASTp protocol.

^f Amino acid identity of first high-scoring segment pair (HSS) %.

^g Homologies based on searching PIR and SWISS-PROT databases (BLASTp nr).

^h Duplicated ORFs located in ITRs.

ⁱ Fragment; complete homologous ORF present in related poxvirus (see reference).

^j Variola India (I) or variola Bangladesh (BSH) sequences; in cases where the variola sequences are not identical, the variola strain first appearing in the blast search protocol is listed.

^k ank, ankyrin.

^l HS, homo sapiens.

^m MM, *Mus musculus*.

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